

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1321	100.0		1321	6	AX392417	Sequence
2	1229	93.0		4839	6	C0812357	Sequence
3	1229	93.0		4839	9	AF305616	Homo sapi
4	1227.4	92.9		1383	6	AX775889	Sequence
5	887.4	67.2		1061	9	BC015918	Homo sapi
6	861	65.2		861	6	AX392419	Sequence
7	803.2	60.8		969	6	BD272494	Secreted
8	802.2	60.7		1141	9	AF234278	Homo sapi
9	801.8	60.7		1913	6	BD272544	Secreted
10	801.6	60.7		969	6	BD272516	Secreted
11	801.6	60.7		969	6	BD272516	Secreted
12	801.6	60.7		969	6	BD272516	Secreted
13	801.6	60.7		1140	6	AX336830	Sequence
14	800.6	60.6		1085	6	AX775887	Sequence
15	800	60.6		1818	9	AY128663	Sequence
16	797.4	60.4		1060	9	BC080635	Homo sapi
17	755.8	57.2		759	6	AX336831	Sequence
18	755.4	57.2		759	6	BD272545	Secreted
19	751.2	56.9		756	6	BD272495	Secreted

Qy	61	CGCGGCGGCGGCGGCGGAGCGCTCGGCTGGGGAAGCTAGGGCAGAGGCTCAGCCCC	120
Db	61		
Qy	121	GGGSGCAGCGCGCGCCGCTGCAGCCCATTTTCCGGAAGCCACCGCGGGCATGCGG	180
Db	121		
Qy	181	ACGCCCCGGGGCTGCGCAGAGGGAGGCGCGGGGGCGCAGCGGAGCGCGTCCGCGCAC	240
Db	181		
Qy	241	TGAGCCCCGGGCGCGCCCGGGAACTTTGGCGCGACCCGAGCCCCGGCGAGCCGGGCGCGC	300
Db	241		
Qy	301	CTCCCCCGCGCGCGCTCTGCTGATGGGGCCCCAGCTCGGGGCGCGCGCGGAGCCCC	360
Db	301		
Qy	361	CCCGGGCGCCCCCGAGCCCCCGCGCCCCCGCGCGCGCGCGCGCTCCATGCAACG	420
Db	361		
Qy	421	CTTGATGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTCTGAC	480
Db	421		
Qy	481	GTGCAACTGCMAACGCTTTTGTTCAGAGCATGAGATCAGGAGCTGGAGTTTGTTC	540
Db	481		
Qy	541	GATCATCATCATCGTGGTGTGATGATGGTGGTGGTGATCAGTGCCTGCTGAG	600
Db	541		
Qy	601	CCACTACAAGCTGTCTGCACGGTCTTTCATCAGCCGGCAGCCAGGGGCGGAGAGAG	660
Db	601		
Qy	661	AGATGCCCTGTCTCAGAAAGATGCCGTGGCCCTCGGAGAGCACAGTGTCAAGCAACG	720
Db	661		
Qy	721	AATCCAGAGCCGAGGTCTACGCCCGCTCGGCCCAACGACCGCTGGCGTGGCGCC	780
Db	721		
Qy	781	CTTGGCCCCAGGGAGCGCTTCCACCGTTTCAGCCCACTATCCGTACTGACGACGA	840
Db	781		
Qy	841	GATCGACTGCACCCACCATCTCGCTGTGAGCGGGAGAGCCCCACCCCTACCAAGG	900
Db	841		
Qy	901	CCCTGCAACCTCGAGTTTCGGGACCCGAGCAGCAGCTGGAATGAACCGGGAGTCCGT	960
Db	901		
Qy	961	GGCGCACCCCCAACAAGACCATCTTTCGACAGTGAACCTGATGATAGTGCAGGCTGG	1020
Db	961		
Qy	1021	CGGCCCCCTGCCCCCAGCAGTAACCTCGGGCATCAGCGCCACGCTGCTACCGCAGCGCGG	1080
Db	1021		
Qy	1081	GGCGATGGAGGGCGCGCGCCACCTTACAGCGAGGTCAATCGGCCACTACCCGGGGTCTC	1140
Db	1081		

QY	1141	CTTCAGACACAGCAGACGAGTGGCGCGCCCTCTCTTCTGCGAGGGAGACCGCGGTCCACCA	1200
Db	1141	CTTTCAGCACACAGCAGACGAGTGGCGCGCCCTCTCTTCTGCGAGGGAGACCGCGGTCCACCA	1200
QY	1201	CACACATATCGCGCCCTTAGAGAGCGCAGACCATCTGGAGCAAAAGAGAAAGATAAACAGAA	1260
Db	1201	CACACATATCGCGCCCTTAGAGAGCGCAGACCATCTGGAGCAAAAGAGAAAGATAAACAGAA	1260
QY	1261	AGGACACCTCTCTAGGGTCCCAAGGGGGCGCGGGCTGGGGCTGCCTAGGTGAAAAGGCA	1320
Db	1261	AGGACACCTCTCTAGGGTCCCAAGGGGGCGCGGGCTGGGGCTGCCTAGGTGAAAAGGCA	1320
QY	1321	G	1321
Db	1321	G	1321
RESULT 2			
CQ812357			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
Wittig, R., Poustka, A., Mollenhauer, J. and Schandendorf, D.			
Target genes for the diagnosis and treatment of cancer			
Patent: WO 2004038020-A 109 06-MAY-2004;			
Deutsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts			
(DE)			
FEATURES			
source			
1. .4839			
/organism="Homo sapiens"			
/mol_type="unassigned DNA"			
/db_xref="taxon:9606"			
misc_feature			
1. .4839			
/note="NM_020182"			
ORIGIN			
Query Match			
Best Local Similarity 100.0%; Pred. No. 2,7e-163;			
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	93	GGAAAGCTAGCGGCAGAGGCTCAGCCCGCGCAGCGCGCGCTGCCAGGCCATT	152
Db	1	GGAAAGCTAGCGGCAGAGGCTCAGCCCGCGCAGCGCGCGCTGCCAGGCCATT	60
QY	153	TTCCGAGCGCACCGCGGGGCACTGCCAGACCCCCCGGGGCTGCCAGGGAGCGGGG	212
Db	61	TTCCGAGCGCACCGCGGGGCACTGCCAGACCCCCCGGGGCTGCCAGGGAGCGGGG	120
QY	213	GGGGCAGCGGAGCGCGTCCCGCGCACTAGACCCCGCGCGCGCCCGGGAACTTGGCGGC	272
Db	121	GGGGCAGCGGAGCGCGTCCCGCGCACTAGACCCCGCGCGCGCCCGGGAACTTGGCGGC	180
QY	273	GACCCGAGCCCGCGAGCGGGGCGCGCTTCCCGCGCGCGCTTCTGCAATGCGGGGC	332
Db	181	GACCCGAGCCCGCGAGCGGGGCGCGCTTCCCGCGCGCGCTTCTGCAATGCGGGGC	240
QY	333	CCGAGCTCCGGGCGCGCGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG	392
Db	241	CCGAGCTCCGGGCGCGCGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG	300
QY	393	GCGCAGCGCGCGCGCTTCCATGCACCGCTTGATGGGGTCAACAGCACGCGCGCGCG	452
Db	301	GCGCAGCGCGCGCGCTTCCATGCACCGCTTGATGGGGTCAACAGCACGCGCGCGCG	360
QY	453	CCGCGGGCAGCCCAATGTCTCTGCAAGCTGCAACTGCAAAACGCTTTGTTCCAGAGCA	512


```
QY 1253 AAACAGAAAGGACACCCCTCTC 1273
Db 841 AAACAGAAAGGACACCCCTCTC 861

RESULT 7
BD272494
LOCUS BD272494 969 bp DNA linear PAT 17-JUL-2003
DEFINITION Secreted proteins and nucleic acids encoding them.
ACCESSION BD272494
VERSION BD272494.1 GI:33082262
KEYWORDS JP 2002539773-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 969)
AUTHORS Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
TITLE Secreted proteins and nucleic acids encoding them
JOURNAL Patent: JP 2002539773-A 3 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002539773-A/3
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/69, PC G01N33/15, G01N33/50, G01N33/53, G01N33/53, G01N33/56, C12N15/00, C12N5/00 CC
PC Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers
FT CDS Location/Qualifiers
source 1..969
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 60.8%; Score 803.2; DB 6; Length 969;
Best Local Similarity 99.6%; Pred. No. 2.1e-103;
Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 514 GGAGATCAGGAGCTGGAGTTCTTCAGATCATCATCATCGTGGTGGTGGTGGTGGT 573
Db 2 GGAGATGGCGGAGCTGGAGTTCTTCAGATCATCATCATCGTGGTGGTGGTGGTGGT 61

QY 574 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 633
Db 62 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121

QY 634 CCGGCAAGCAGCAGGCGGAGGAGAGAGAGTGCCTGTCTCAGAGAGTGCCTGTGGCC 693
Db 122 CCGGCAAGCAGCAGGCGGAGGAGAGAGAGTGCCTGTCTCAGAGAGTGCCTGTGGCC 181

QY 694 CTGGAGAGCAGAGTGTGAGGCAACCGAATCCAGAGCCGAGGTCTACGCCCGGCTCG 753
Db 182 CTGGAGAGCAGAGTGTGAGGCAACCGAATCCAGAGCCGAGGTCTACGCCCGGCTCG 241

QY 754 GCCACCGAGCGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCT 813
Db 242 GCCACCGAGCGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCT 301

QY 814 GCCACCTATCCGTACCTGAGCAGAGATCGACCTGCCACCCACCATCTCGTGTGAGA 873
Db 302 GCCACCTATCCGTACCTGAGCAGAGATCGACCTGCCACCCACCATCTCGTGTGAGA 361

QY 874 CGGGAGGAGCCCGCCACCTTACAGAGGCGCCCTGACCTCCAGCTTCGGAGCCCGAGCA 933
Db 362 CGGGAGGAGCCCGCCACCTTACAGAGGCGCCCTGACCTCCAGCTTCGGAGCCCGAGCA 421
```

```
QY 934 GCAGCTGGAACTGAACCGGAGTTCGGTGGCGCACCCCAACAGAACCATCTTCGACAG 993
Db 422 GCAGCTGGAACTGAACCGGAGTTCGGTGGCGCACCCCAACAGAACCATCTTCGACAG 481

QY 994 TGACCTGATGGATAGTGCAGGCTGGCGGCGCCCTGCCCCCCCCCAGAGTAACCTCGGCGCAT 1053
Db 482 TGACCTGATGGATAGTGCAGGCTGGCGGCGCCCTGCCCCCCCCCAGAGTAACCTCGGCGCAT 541

QY 1054 CAGCGCCACGTGTCTACGCGCAGCGCGCGCGCATGAGGGGCGCCGCCACCTACAGCGA 1113
Db 542 CAGCGCCACGTGTCTACGCGCAGCGCGCGCGCATGAGGGGCGCCGCCACCTACAGCGA 601

QY 1114 GGTCTATGGCCACTACCCGGGTCCTCTTCAGACACCGAGCAGAGTGGGGCGCCCTC 1173
Db 602 GGTCTATGGCCACTACCCGGGTCCTCTTCAGACACCGAGCAGAGTGGGGCGCCCTC 661

QY 1174 CTTGCTGGAGGGGACCCGGCTCCACACACACATCGGCGCCCTTAGAGAGCCGAGCAT 1233
Db 662 CTTGCTGGAGGGGACCCGGCTCCACACACACATCGGCGCCCTTAGAGAGCCGAGCAT 721

QY 1234 CTGGAGCAAGAGAGAGTAAACAGAAAGGACACACCTCTCTAGGGTCCCCCAGGGGGCGG 1293
Db 722 CTGGAGCAAGAGAGAGTAAACAGAAAGGACACACCTCTCTAGGGTCCCCCAGGGGGCGG 781

QY 1294 GGCTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1321
Db 782 GGCTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 809

RESULT 8
AF224278 1141 bp mRNA linear PRI 18-JUL-2000
LOCUS Homo sapiens PMEPA1 protein (PMEPA1) mRNA, complete cds.
DEFINITION
ACCESSION AF224278
VERSION AF224278.1 GI:9255808
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1141)
AUTHORS Xu,L.L., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLeod,D.G., Moul,J.W. and Srivastava,S.
TITLE A novel androgen-regulated gene, PMEPA1, located on chromosome 20q13 exhibits high level expression in prostate
JOURNAL Genomics 66 (3), 257-263 (2000)
MEDLINE 20334621
PUBMED 10873380
REFERENCE 2 (bases 1 to 1141)
AUTHORS Xu,L.L., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLeod,D.G., Moul,J.W. and Srivastava,S.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) CPDR, USUHS, 1530 East Jefferson Street, Rockville, MD 20852, USA
FEATURES
Location/Qualifiers
source 1..1141
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosomes="20"
/map="20q13.31-13.33"
/cell_line="LNCap"
1..1141
/genes="PMEPA1"
96..854
/genes="PMEPA1"
/notes="type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostate glandular epithelial cells; similar to the predicted protein encoded by sequence deposited at GenBank Accession Number NP_004329"
```



```
/codon_start=1
/product="PMEP1 protein"
/protein_id="AAF86322.1"
/db_xref="GI:9255809"
/translation="MAELSEFVOLIIVVMVMMVVITCLSHYKLSAHSFISRHQS
RRREDALSEGCLWPSESTVSGNGIEPQVYAPPRTRDLAVPPFAQRERFRHFQTY
PYLQHEIDLPPTLSLSDGEPPEPYQGLTQLRDPEQLNRESVRAPNRTIFDSD
LMSDALRGFCPPSSNGISATCYGSGGMEGPPPTYSVIGHYPGSSPQHOSSGPP
SILLEGTRLHHTHAPLESAAINSEKDKQKQHPL"

ORIGIN
Query Match      60.7%; Score 802.2; DB 9; Length 1141;
Best Local Similarity 98.4%; Pred. No. 2.8e-103;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 499 TTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTGTTGATCATCATCATCATCGTGGT 558
Db 77 TCTCTCGGNAACAGCAATGGCGAGCTGGAGTTGTTGATCATCATCATCATCGTGGT 136

QY 559 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 618
Db 137 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 196

QY 619 ACAGTCTTTCATCAGCGGACAGCAGCGGCGGAGAGAGAGATGCTGCTCTCAGA 678
Db 197 ACAGTCTTTCATCAGCGGACAGCAGCGGCGGAGAGAGATGCTGCTCTCAGA 256

QY 679 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 738
Db 257 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGCAAGT 316

QY 739 CTACGCGCGCGCTCGGCGCCACCGACCGCTGCGCGCGCGCTGCGCGCGCGCGCGCG 798
Db 317 CTACGCGCGCGCTCGGCGCCACCGACCGCTGCGCGCGCGCTGCGCGCGCGCGCGCG 376

QY 799 CTTCCACCGCTTCAGCGCCACCTATCGGTACCTGACGACGAGATCGAAGCTGCAACCCAC 858
Db 377 CTTCCACCGCTTCAGCGCCACCTATCGGTACCTGACGACGAGATCGAAGCTGCAACCCAC 436

QY 859 CATCTCGCTGTAGAGGGGAGAGCGCCACCGCTACCGGGCGCGCGCGCGCGCGCGCG 918
Db 437 CATCTCGCTGTAGAGGGGAGAGCGCCACCGCTACCGGGCGCGCGCGCGCGCGCGCG 496

QY 919 TCGGAGACCGCGAGCAGCTGGAACCTGACCGGGAGTGGTGGCGGCGACCCCAACAG 978
Db 497 TCGGAGACCGCGAGCAGCTGGAACCTGACCGGGAGTGGTGGCGGCGACCCCAACAG 556

QY 979 AACCATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1038
Db 557 AACCATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 616

QY 1039 CAGTAACCTGGGCATCAGCGCCACGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1098
Db 617 CAGTAACCTGGGCATCAGCGCCACGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 676

QY 1099 GCCCACTACAGCGAGTCACTCGGCCACTACCGCGGGTCTCTCTCCAGCACGAGAGAG 1158
Db 677 GCCCACTACAGCGAGTCACTCGGCCACTACCGCGGGTCTCTCTCCAGCACGAGAGAG 736

QY 1159 CAGTGGCGCGCTCTCTTGTGAGGGGACCGCGCTCCACCAACACATGCGCGCGCT 1218
Db 737 CAGTGGCGCGCTCTCTTGTGAGGGGACCGCGCTCCACCAACACATGCGCGCGCT 796

QY 1219 AGAGCGGAGCATCTGGAGCAAGAGAGAGATTAACAGAGAGAGAGAGAGAGAGAGAGAG 1278
Db 797 AGAGCGGAGCATCTGGAGCAAGAGAGAGATTAACAGAGAGAGAGAGAGAGAGAGAGAG 856

QY 1279 TCCCGAGGGGGCGCGGCTGGGCTGCTAGGTGAAAGAGAGAGAGAGAGAGAGAGAGAG 1321
Db 857 TCCCGAGGGGGCGCGGCTGGGCTGCTAGGTGAAAGAGAGAGAGAGAGAGAGAGAGAG 899

FEATURES
source
1..1913
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      60.7%; Score 801.8; DB 6; Length 1913;
Best Local Similarity 98.3%; Pred. No. 2.8e-103;
Matches 809; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 499 TTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTGTTGATCATCATCATCATCGTGGT 558
Db 127 TCTCTCGGNAACAGCAATGGCGAGCTGGAGTTGTTGATCATCATCATCATCGTGGT 186

QY 559 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 618
Db 187 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 246

QY 619 ACAGTCTTTCATCAGCGGACAGCAGCGGCGGAGAGAGATGCTGCTCTCAGA 678
Db 247 ACAGTCTTTCATCAGCGGACAGCAGCGGCGGAGAGAGATGCTGCTCTCAGA 306

QY 679 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGCAAGT 738
Db 307 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGT 366

QY 739 CTACGCGCGCGCTCGGCGCCACCGACCGCTGCGCGCGCGCTGCGCGCGCGCGCGCG 798
Db 367 CTACGCGCGCGCTCGGCGCCACCGACCGCTGCGCGCGCGCTGCGCGCGCGCGCGCG 426

QY 799 CTTCCACCGCTTCAGAGCGGAGAGCGCCACCGCTACGAGCAGAGATCGAAGCTGCAACCCAC 858
Db 427 CTTCCACCGCTTCAGAGCGGAGAGCGCCACCGCTACGAGCAGAGATCGAAGCTGCAACCCAC 486

QY 859 CATCTCGCTGTAGAGGGGAGAGCGCCACCGCTACGAGGCGCGCGCGCGCGCGCGCG 918
Db 487 CATCTCGCTGTAGAGGGGAGAGCGCCACCGCTACGAGGCGCGCGCGCGCGCGCGCG 546

QY 919 TCGGAGACCGCGAGCAGCTGGAACCTGAGAGTGGTGGCGGAGAGAGAGAGAGAGAG 978
Db 547 TCGGAGACCGCGAGCAGCTGGAACCTGAGAGTGGTGGCGGAGAGAGAGAGAGAGAG 606

QY 979 AACCATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1038
```


Db	607	TTCGACAGTACCTGATGATAGTCAGGCTGGGCGCCCTCTGCCCCCAG	666
Qy	1039	CAGTAACCTGGGATCAGCGCCACGCTGCTACGCGCAGCGCGCGCGCATGAGGCGCGCC	1098
Db	667	CAGTAACCTGGGATCAGCGCCACGCTGCTACGCGCAGCGCGCGCGCATGAGGCGCGCC	726
Qy	1099	GCCCACTTACAGGAGGTATCTGCGCAGCTACCCCGGGTCTCTTCCAGACACGAGAG	1158
Db	727	GCCCACTTACAGGAGGTATCTGCGCAGCTACCCCGGGTCTCTTCCAGACACGAGAG	786
Qy	1159	CAGTGGCGCGCCCTCTCTGCGAGGGGACCGGCTCCACACACACATCGCGCCCT	1218
Db	787	CAGTGGCGCGCCCTCTCTGCGAGGGGACCGGCTCCACACACACATCGCGCCCT	846
Qy	1219	AGAGAGCGAGCCATCTGAGGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGG	1278
Db	847	AGAGAGCGAGCCATCTGAGGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGG	906
Qy	1279	TCCCCAGGGGCGCGGCTGGGCTGCGTAGGTGAAAGGCAG	1321
Db	907	TCCCCAGGGGCGCGGCTGGGCTGCGTAGGTGAAAGGCAG	949
RESULT 10			
LOCUS	BD272514	969 bp	DNA linear
DEFINITION	Secreted proteins and nucleic acids encoding them.		
ACCESSION	BD272514		
VERSION	BD272514.1	GI:33082282	
KEYWORDS	JP 2002539773-A/23.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 969)		
JOURNAL	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.		
COMMENT	Secreted proteins and nucleic acids encoding them		
	Patent: JP 2002539773-A 23 26-NOV-2002;		
	MILLENNIUM PHARMACEUTICALS INC		
	OS Homo sapiens (human)		
	PN JP 2002539773-A/23		
	PF 26-NOV-2002		
	PP 01-MAR-2000 JP 2000602247		
	PR 01-MAR-1999 US 60/122458		
	PI THOMAS M BARNES,DOUGLAS A HOLTZMAN, JOHN D SHARP,CHRISTOPHER C		
	PI FRASER		
	PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC		
	GOIN33/15,		
	PC GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566,C12N15/00,C12N5/00 CC		
	Secreted proteins and nucleic acids encoding them FH Key		
FEATURES	Location/Qualifiers	(6). (761).	
source	1. .969		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
ORIGIN	Query Match 60.7%; Score 801.6; DB 6; Length 969;		
	Best Local Similarity 99.5%; Pred. No. 3.4e-103;		
	Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
Qy	514	GGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGTGTGATGTGAT	573
Db	2	GGAGATGCGCGGACCTGGAGTTGTTTCAGATCATCATCATCGTGGTGTGATGTGAT	61
Qy	574	GGTGGTGGTGTATCATCGTCTGCTGAGGCCACTACAAGCTGTCTGACGGTCTTTCATCAG	633
Db	62	GGTGGTGGTGTATCATCGTCTGCTGAGGCCACTACAAGCTGTCTGACGGTCTTTCATCAG	121
Qy	634	CCGGCACAGCCAGGGGCGGAGGAGAGATGCCCTGTCTCAGAGAGGATGCCGTGTGGCC	693
Db	122	TTCGACAGTACCTGATGATAGTCAGGCTGGGCGCCCTCTGCCCCCAG	181
Qy	694	CAGTAACCTGGGATCAGCGCCACGCTGCTACGCGCAGCGCGCGCGCATGAGGCGCGCC	753
Db	182	CAGTAACCTGGGATCAGCGCCACGCTGCTACGCGCAGCGCGCGCGCATGAGGCGCGCC	241
Qy	754	GCCCACTTACAGGAGGTATCTGCGCAGCTACCCCGGGTCTCTTCCAGACACGAGAG	813
Db	242	GCCCACTTACAGGAGGTATCTGCGCAGCTACCCCGGGTCTCTTCCAGACACGAGAG	301
Qy	814	GCCCACTTACAGGAGGTATCTGCGCAGCTACCCCGGGTCTCTTCCAGACACGAGAG	873
Db	302	GCCCACTTACAGGAGGTATCTGCGCAGCTACCCCGGGTCTCTTCCAGACACGAGAG	361
Qy	874	CGGGGAGGAGCCCGCCACCTTACAGGGCGCCCTGACCCCTCCAGCTTCGGGACCCCGGCA	933
Db	362	CGGGGAGGAGCCCGCCACCTTACAGGGCGCCCTGACCCCTCCAGCTTCGGGACCCCGGCA	421
Qy	934	GCAGCTGGAACTGAAACCGGGAGTCTGGTGGCGGCACCCCCAACAGAACCATCTTCGACAG	993
Db	422	GCAGCTGGAACTGAAACCGGGAGTCTGGTGGCGGCACCCCCAACAGAACCATCTTCGACAG	481
Qy	994	TGACCTGATGGATAGTCCAGGCTGGGCGGCGCCCTGCGGCGGCGGCGGCGGCGGCGGCGG	1053
Db	482	TGACCTGATGGATAGTCCAGGCTGGGCGGCGCCCTGCGGCGGCGGCGGCGGCGGCGGCGG	541
Qy	1054	CAGCGCCAGCTGCTACGCGCAGCGGGCGGCGCATGAGAGGGCGGCGGCGGCGGCGGCGGCGG	1113
Db	542	CAGCGCCAGCTGCTACGCGCAGCGGGCGGCGCATGAGAGGGCGGCGGCGGCGGCGGCGGCGG	601
Qy	1114	GGTCATCGGCCACTACCGGGGCTCTCTTCCAGCACCAGCAGAGAGAGAGAGAGAGAGAGAGAG	1173
Db	602	GGTCATCGGCCACTACCGGGGCTCTCTTCCAGCACCAGCAGAGAGAGAGAGAGAGAGAGAGAG	661
Qy	1174	CTTCTGAGGAGGAGCCCGGCTCCACACACACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1233
Db	662	CTTCTGAGGAGGAGCCCGGCTCCACACACACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	721
Qy	1234	CTGGAGCAAGAGAGAGGATAAAACAGAAAGGACACCCCTCTCTAGGGTCCCCCAGGGGCGCGG	1293
Db	722	CTGGAGCAAGAGAGAGGATAAAACAGAAAGGACACCCCTCTCTAGGGTCCCCCAGGGGCGCGG	781
Qy	1294	GGCTGGGCTGCTAGGTGAAAAGGCAG	1321
Db	782	GGCTGGGCTGCTAGGTGAAAAGGCAG	809
RESULT 11			
LOCUS	BD272515	969 bp	DNA linear
DEFINITION	Secreted proteins and nucleic acids encoding them.		
ACCESSION	BD272515		
VERSION	BD272515.1	GI:33082283	
KEYWORDS	JP 2002539773-A/24.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 969)		
JOURNAL	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.		
COMMENT	Secreted proteins and nucleic acids encoding them		
	Patent: JP 2002539773-A 24 26-NOV-2002;		
	MILLENNIUM PHARMACEUTICALS INC		
	OS Homo sapiens (human)		
	PN JP 2002539773-A/24		
	PP 26-NOV-2002		
	PF 01-MAR-2000 JP 2000602247		
	PR 01-MAR-1999 US 60/122458		
	PI THOMAS M BARNES,DOUGLAS A HOLTZMAN, JOHN D SHARP,CHRISTOPHER C		
	PI FRASER		
	PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC		
	GOIN33/15,		
	PC GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566,C12N15/00,C12N5/00 CC		
	Secreted proteins and nucleic acids encoding them FH Key		
FEATURES	Location/Qualifiers	(6). (761).	
source	1. .969		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
ORIGIN	Query Match 60.7%; Score 801.6; DB 6; Length 969;		
	Best Local Similarity 99.5%; Pred. No. 3.4e-103;		
	Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
Qy	514	GGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGTGTGATGTGAT	573
Db	2	GGAGATGCGCGGACCTGGAGTTGTTTCAGATCATCATCATCGTGGTGTGATGTGAT	61
Qy	574	GGTGGTGGTGTATCATCGTCTGCTGAGGCCACTACAAGCTGTCTGACGGTCTTTCATCAG	633
Db	62	GGTGGTGGTGTATCATCGTCTGCTGAGGCCACTACAAGCTGTCTGACGGTCTTTCATCAG	121
Qy	634	CCGGCACAGCCAGGGGCGGAGGAGAGATGCCCTGTCTCAGAGAGGATGCCGTGTGGCC	693

Db 482 TGACCTGATGATAGTCCAGGCTGGCGGCCCTGCCCCCAGCAGTAACCTCGGGCAT 541

Qy 1054 CAGCGCCACGTGCTACCGGAGCGCGGCGGCATAGAGGGGCCCGCCACCTACAGCGA 1113

Db 542 CAGCGCCACGTGCTACCGGAGCGCGGCGGCATAGAGGGGCCCGCCACCTACAGCGA 601

Qy 1114 GGTCACTGGCCACTACCGGGGTCTCTTCCAGCACCCAGCAGAGTGGCGGCCCTC 1173

Db 602 GGTCACTGGCCACTACCGGGGTCTCTTCCAGCACCCAGCAGAGTGGCGGCCCTC 661

Qy 1174 CTTGCTGGAGGGACCGCGCTCCACACACACATCGCGCCCTTAGAGAGCCAGCCAT 1233

Db 662 CTTGCTGGAGGGACCGCGCTCCACACACACATCGCGCCCTTAGAGAGCCAGCCAT 721

Qy 1234 CTGGAGCAAGAGAGGATAAACAGAAAGGACACCTCTTAGGGTCCCCAGGGGGCCG 1293

Db 722 CTGGAGCAAGAGAGGATAAACAGAAAGGACACCTCTTAGGGTCCCCAGGGGGCCG 781

Qy 1294 GGTGGGGTGGCTAGGTGAAAGGCAG 1321

Db 782 GGTGGGGTGGCTAGGTGAAAGGCAG 809

RESULT 13

AR336830

LOCUS AR336830 1140 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 1 from patent US 6566130.

ACCESSION AR336830

VERSION AR336830.1 GI:33722680

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1140)

AUTHORS Srivastava, S., Moul, J. W., Xu, L. L. and Segawa, T.

TITLE Androgen-regulated gene expressed in prostate tissue

JOURNAL Patent: US 6566130-A 1 20-MAY-2003;

FEATURES

source

1. .1140

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 60.7%; Score 801.6; DB 6; Length 1140;

Best Local Similarity 99.5%; Pred. No. 3.3e-103;

Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 514 GGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGT 573

Db 91 GGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGT 150

Qy 574 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 633

Db 151 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 210

Qy 634 CCGGCACAGCAGGGCGGAGGAGAGAGTCCCTGTCTCAGAAAGGATGCCTGTGGCC 693

Db 211 CCGGCACAGCAGGGCGGAGGAGAGAGTCCCTGTCTCAGAAAGGATGCCTGTGGCC 270

Qy 694 CTCGGAGAGCAGTGTGAGGCAACGGAATCCAGAGCCAGAGTCTACGCCCGCGCTCG 753

Db 271 CTCGGAGAGCAGTGTGAGGCAACGGAATCCAGAGCCAGAGTCTACGCCCGCGCTCG 330

Qy 754 GCCCAGCCAGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGCA 813

Db 331 GCCCAGCCAGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGCA 390

Qy 814 GCCCAGCTATCCGTACCTGAGCAGCAGATCGACCTGCCACCCACCATCTCGTGTGAGA 873

Db 391 GCCCAGCTATCCGTACCTGAGCAGCAGATCGACCTGCCACCCACCATCTCGTGTGAGA 450

Qy 874 CGGGAGGAGCCCGCCACCTTACAGGGGCCCTCGACCTTCAGCTTCGGAGCCCGGAGCA 933

Db 451 CGGGGAGGAGCCCCACCTACAGGGGCCCTGCACTCCAGCTTCGGGACCCCGAGCA 510

Qy 934 GCAGCTGGAACCTGAAACCGGAGTCTGGTGGCGCACCCCCAAAACAGAACCACTCTTCGACAG 993

Db 511 GCAGCTGGAACCTGAAACCGGAGTCTGGTGGCGCACCCCCAAAACAGAACCACTCTTCGACAG 570

Qy 994 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053

Db 571 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 630

Qy 1054 CAGCGCCACCTGCTACCGGAGCGCGGCGGCATGAGAGGGGCCCGCCACCTACAGCGA 1113

Db 631 CAGCGCCACCTGCTACCGGAGCGCGGCGGCATGAGAGGGGCCCGCCACCTACAGCGA 690

Qy 1114 GGTCACTGGCCACTACCGGGGTCTCTTCCAGCACCCAGCAGAGTGGCGGCCCTC 1173

Db 691 GGTCACTGGCCACTACCGGGGTCTCTTCCAGCACCCAGCAGAGTGGCGGCCCTC 750

Qy 1174 CTTGCTGGAGGGACCGCGCTCCACACACACATCGCGCCCTTAGAGAGCCAGCCAT 1233

Db 751 CTTGCTGGAGGGACCGCGCTCCACACACACATCGCGCCCTTAGAGAGCCAGCCAT 810

Qy 1234 CTGGAGCAAGAGAGGATAAACAGAAAGGACACACCTCTTAGGGTCCCCAGGGGGCCG 1293

Db 811 CTGGAGCAAGAGAGGATAAACAGAAAGGACACACCTCTTAGGGTCCCCAGGGGGCCG 870

Qy 1294 GGTGGGGTGGCTAGGTGAAAGGCAG 1321

Db 871 GGTGGGGTGGCTAGGTGAAAGGCAG 898

RESULT 14

AX775887

LOCUS AX775887 1085 bp mRNA linear PAT 14-JUL-2003

DEFINITION Sequence 157 from Patent WO03048202.

ACCESSION AX775887

VERSION AX775887.1 GI:32693605

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Matsuda, A. and Muramatsu, S.

TITLE NF- κ B activating gene

JOURNAL Patent: WO 03048202-A 157 12-JUN-2003;

Asahi Kasei Kabushiki Kaisha (JP)

FEATURES

source

1. .1085

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

128_886

/notes="unlabeled protein product"

/codon_start=1

/protein_id="CAE11643.1"

/db_xref="GI:32693606"

/translation="MALEFVQIIIVVMVVMVVITCLLSHYKLSARSFISRHSGQ
RRRDLASSEGLWPSESTVSGNIGIPEOVYAPRPTDLRLAVPPAQRERFHRFOPT
PYLQHEIDLPPTISLDSEPPYQGPCTQLRLDPEQOLELNRESVAPRNRTFDS
LMDARKLGCPFPSSNSGISATCYGSGRNEGPPPTIYSEVIGHYPSGSSFOHQSSGFP
SLLEGLRHLTHIAPLESAAIWSKEKDKQKHPL"

ORIGIN

Query Match 60.6%; Score 800.6; DB 6; Length 1085;

Best Local Similarity 98.3%; Pred. No. 4.7e-103;

Matches 809; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 499 TTGTGTTCCAGAGCATGGAGATCAGGAGTGGAGTTTGTTCAGATCATCATCGTGGT 558

Db 109 TCTCTCGGAAACAGGAGCATGGCGAGTGGAGTTTGTTCAGATCATCATCGTGGT 168

Qy 559 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 618

[illegible]

This Page Blank (uspro)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 00:48:19 ; Search time 707.116 Seconds
(without alignments)
11058.969 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcggagcga.....ctgcgtagtgaaaggcag 1321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	6	Abk12137 Human cdn
2	1301	98.5	4911	13	Acc40804 Tumour-as
3	1229	93.0	4839	8	Acc49552 Tumour-as
4	1229	93.0	4839	11	Adp65809 Human STA
5	1229	93.0	4839	11	Adp65729 Human tra
6	1229	93.0	4839	12	Adm67045 Human hom
7	1229	93.0	4839	13	Adr65875 Human pro
8	1229	93.0	4839	13	Adr66778 Human pro
9	1227.4	92.9	1383	10	Adc37326 Nuclear f
10	864	65.4	864	11	Adn38809 Cancer/an
11	803.2	60.8	969	3	Aaa75151 cDNA enco
12	802.2	60.7	1140	6	Abk92120 Prostate
13	802.2	60.7	1141	10	Adb75588 Prostate
14	802.2	60.7	1850	8	Acc49536 Tumour-as
15	802.2	60.7	4527	11	Adl83313 Human and
16	801.6	60.7	969	3	Aaa75164 cDNA clon
17	801.6	60.7	969	3	Aaa75163 cDNA clon
18	801.6	60.7	969	3	Aaa75165 cDNA clon
19	801.6	60.7	1140	10	Ado60105 Human and
20	801.6	60.7	1140	10	Adh62276 Human PME

21	801.6	60.7	1140	12	Ado39826	Ado39826 Human PME
22	800.6	60.6	1061	3	AAA47429	Aaa47429 Sequence
23	800.6	60.6	1085	10	ADC37324	Adc37324 Nuclear f
24	800.6	60.6	1334	8	ABZ36103	Abz36103 Human sec
25	790.4	59.8	1066	4	AAI57868	Aai57868 Human pol
26	767.4	58.1	806	4	ACC49537	Acc49537 Tumour-as
27	760	57.5	1069	4	AAI59654	Aai59654 Human pol
28	755.8	57.2	759	10	ADP17545	Adp17545 Human and
29	755.8	57.2	759	10	ADH62277	Adh62277 Human PME
30	755.8	57.2	759	12	ADO39827	Ado39827 Human PME
31	616.4	46.7	878	6	ABK12142	Abk12142 Mouse cdn
32	589.2	44.6	1583	6	ABSG61424	Absg61424 Prostate
33	493.6	37.4	693	6	ABK12143	Abk12143 Human MIV
34	466.2	35.3	1713	3	AAA75152	Aaa75152 cDNA enco
35	464.6	35.2	1713	3	AAA75167	Aaa75167 cDNA clon
36	464.6	35.2	1713	3	AAA75166	Aaa75166 cDNA clon
37	464.6	35.2	1713	3	AAA75168	Aaa75168 cDNA clon
38	417.8	31.6	812	2	AAZ52964	Aaz52964 Human pro
39	417	31.6	474	10	ABZ84732	Abz84732 Toxicolog
40	410.8	31.1	711	12	ADO00336	Ado00336 Novel hum
41	410.8	31.1	711	12	ADN98767	Adn98767 Novel hum
42	401.4	30.4	408	5	AAF65983	Aaf65983 Novel hum
43	400.6	30.3	673	6	ABT09178	Abt09178 Phase-1 R
44	400.6	30.3	673	12	ADG45576	Adg45576 Liver inf
45	400.6	30.3	673	12	ADH22874	Adh22874 Partial D

ALIGNMENTS

RESULT 1
ABK12137
ID ABK12137 standard; cDNA; 1321 BP.
XX
AC ABK12137;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
XX
KW Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
KW cytoskeletal; cardiant; cerebroprotective; antiarteriosclerotic;
KW cardiac cell; anti-apoptotic; vascular endothelial cell;
KW heart hypertrophy; myocardial infarction; stroke; arteriosclerosis;
KW heart failure.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 413..1276
FT /*tag= a
FT /product= "MIVR-1"
FT /note= "This region is specifically claimed in claim 3"
XX
XX WO200216416-A2.
XX
XX 28-FEB-2002.
XX
XX 21-AUG-2001; 2001WO-US026089.
XX
XX 22-AUG-2000; 2000US-0227159P.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX (PFIZ) PFIZER INC.
XX
XX Lee RT, Landschulz KT, Kennedy SP, Thompson JP, Turi TG;
XX WPI; 2002-280912/32.
XX P-PSDB; AAU78231.
XX
XX Novel nucleic acid molecule encoding Mechanically Induced Vascular
XX Receptor-1 polypeptide, useful for treating cardiovascular diseases.
XX

Claim 2; Page 87-88; 105pp; English.

The invention relates to an isolated nucleic acid molecule encoding a Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having a cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences A1761441.1, A1594390, NM 004338 and A0177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IEX-1, VDP-1, BFG-2 and TIS-1 or its expression product, determining if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and disorders as characterized by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart failure. The present sequence encodes human MIVR-1

Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 1321; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 2.6e-198;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGCGTCTCGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGG 60
DB 1 CGACCGCGTCTCGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGG 60
QY 61 CGGCGGCGGCGGCGGCGGCGCTCGCTGGGAAAGCTAGCGGAGGCTCAGCCCC 120
DB 61 CGGCGGCGGCGGCGGCGGCGCTCGCTGGGAAAGCTAGCGGAGGCTCAGCCCC 120
QY 121 GGGCGAGCGCGCGCGCGCTGCGAGCCCATTTTCGGAGCGCCACCGCGGCACTGCCG 180
DB 121 GGGCGAGCGCGCGCGCGCTGCGAGCCCATTTTCGGAGCGCCACCGCGGCACTGCCG 180
QY 181 ACGCCCCCGGGGTCGCGAGGAGGCGCGGGGGCGCAGCGAGCGCGTCCCGCGCAC 240
DB 181 ACGCCCCCGGGGTCGCGAGGAGGCGCGGGGGCGCAGCGAGCGCGTCCCGCGCAC 240
QY 241 TGAGCCCCCGGCGCGCGCGGAACTTGGCGGCGACCGCGGCGGCGGCGGCGCGC 300
DB 241 TGAGCCCCCGGCGCGCGCGGAACTTGGCGGCGACCGCGGCGGCGGCGGCGCGC 300
QY 301 CTCCCCCGCGCGCGCTCTCTGATCGGGGCGCCAGCTCCGGGCGCGCGCGGCGCC 360
DB 301 CTCCCCCGCGCGCGCTCTCTGATCGGGGCGCCAGCTCCGGGCGCGCGCGGCGCC 360
QY 361 CCG 420
DB 361 CCG 420
QY 421 CTTGATGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 421 CTTGATGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 GTGCAACTGCAACCGCTCTTTGTCAGAGCATGAGATCAGGAGCTGGAGTTGTTC 540
DB 481 GTGCAACTGCAACCGCTCTTTGTCAGAGCATGAGATCAGGAGCTGGAGTTGTTC 540
QY 541 GATCATCATCATCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 541 GATCATCATCATCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 601 CCACTAAGCTGTCTGCAAGCTCTTTCATAGCGCGCGCACAGCGGCGGAGGAGAGA 660
DB 601 CCACTAAGCTGTCTGCAAGCTCTTTCATAGCGCGCGCACAGCGGCGGAGGAGAGA 660
QY 661 AGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGAGCACAGTGTGAGCAACGG 720
DB 661 AGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGAGCACAGTGTGAGCAACGG 720

QY 721 AATCCAGAGCGGAGGCTCTACGCCCGCGCTCGGCCCAACCGACCGCTGCGCTGCCGCC 780
DB 721 AATCCAGAGCGGAGGCTCTACGCCCGCGCTCGGCCCAACCGACCGCTGCGCTGCCGCC 780
QY 781 CTTGCGCCAGCGGAGCGGCTTCCACCGCTTCAGCGCCACCTATCCGTACTGACAGACGA 840
DB 781 CTTGCGCCAGCGGAGCGGCTTCCACCGCTTCAGCGCCACCTATCCGTACTGACAGACGA 840
QY 841 GATCGACCTGCGCACCCACCATCTCGCTGTTCAGACGGGAGGAGCGCCACCTTACCAGG 900
DB 841 GATCGACCTGCGCACCCACCATCTCGCTGTTCAGACGGGAGGAGCGCCACCTTACCAGG 900
QY 901 CCCTTCACCTTCAGCTTCGGGACCCCGAGCAGCAGTGTGAACCCGGAGTCGCT 960
DB 901 CCCTTCACCTTCAGCTTCGGGACCCCGAGCAGCAGTGTGAACCCGGAGTCGCT 960
QY 961 GCGCGCACCCCGCAAAACAGAACCATCTTCGACAGTGTGACCTGATGGATAGTCCAGGCTGG 1020
DB 961 GCGCGCACCCCGCAAAACAGAACCATCTTCGACAGTGTGACCTGATGGATAGTCCAGGCTGG 1020
QY 1021 CGGCGCTTCGCCCGCCAGCAGTAATCTCGGGCATCAGCGCCACGTCTACGGCAGCGGCG 1080
DB 1021 CGGCGCTTCGCCCGCCAGCAGTAATCTCGGGCATCAGCGCCACGTCTACGGCAGCGGCG 1080
QY 1081 GCGCATGAGGAGGCGCGCGCCACCTTACAGCGAGGTCATCGGCCACTACCCGGGTCCTC 1140
DB 1081 GCGCATGAGGAGGCGCGCGCCACCTTACAGCGAGGTCATCGGCCACTACCCGGGTCCTC 1140
QY 1141 CTTCCAGCACCGAGCAGTGGCGCGCTTCCTTCCTGAGGAGGACCCCGCTCCACCA 1200
DB 1141 CTTCCAGCACCGAGCAGTGGCGCGCTTCCTTCCTGAGGAGGACCCCGCTCCACCA 1200
QY 1201 CACACATCGCGCGCTTACAGAGCGGAGCGGACCATCTGAGAGCAAGAGAGGATAACAGAA 1260
DB 1201 CACACATCGCGCGCTTACAGAGCGGAGCGGACCATCTGAGAGCAAGAGAGGATAACAGAA 1260
QY 1261 AGGACACCTCTCTTAGGCTCCCGAGGCGCGCGCTGCGTAGGTGAAAGGCA 1320
DB 1261 AGGACACCTCTCTTAGGCTCCCGAGGCGCGCGCTGCGTAGGTGAAAGGCA 1320
QY 1321 G 1321
DB 1321 G 1321

RESULT 2
ACN40804
ID ACN40804 standard; cDNA; 4911 BP.
XX ACN40804;
XX ACN40804;
DT 18-NOV-2004 (first entry)
XX Tumour-associated antigenic target (TAT) | cDNA DNA326860, SEQ ID NO:5823.
DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic; gene; ss.
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX

PA (GETH) GENENTECH INC.
XX Wu TD, Zhang Z, Zhou Y;
XX MPI; 2004-347921/32.
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 1; SEQ ID NO 5823; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX
SQ Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;

Query Match 98.5%; Score 1301; DB 13; Length 4911;
Best Local Similarity 100.0%; Pred. No. 3.3e-195;
Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AACCCGATCTCTTGGACTTGAATGAGGAGGAGGCGGCGCGCGCGCGCGGAG 80
DB 1 AACCCGATCTCTTGGACTTGAATGAGGAGGAGGCGGCGCGCGCGCGGAG 60

QY 81 GCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCCCGCGGAGCGCGCCCCGC 140
DB 61 GCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCCCGCGGAGCGCGCCCCGC 120

QY 141 TGCAGCCCATTTTCCGAGCGCCACCGCGGAGCACTGCCGAGCGCCCCCGGCGTCCGAG 200
DB 121 TGCAGCCCATTTTCCGAGCGCCACCGCGGAGCACTGCCGAGCGCCCCCGGCGTCCGAG 180

QY 201 GGGAGCGCGGGGGGCGCAGCGAGCGCGTCCCGGCGCACTGAGCGCCCGGCGCCCCCG 260
DB 181 GGGAGCGCGGGGGGCGCAGCGAGCGCGTCCCGGCGCACTGAGCGCCCGGCGCCCCCG 240

QY 261 GAATTTGGGGCGCACCGAGCGCGCGGCGCGCTCCCGCGCGCGCGCTCC 320
DB 241 GAATTTGGGGCGCACCGAGCGCGCGGCGCGCTCCCGCGCGCGCGCTCC 300

QY 321 TGCATGCGGGGCGCCAGCTCCGGGCGCGCGCGGAGCGCCCCCGCGCGCGCGCGCC 380
DB 301 TGCATGCGGGGCGCCAGCTCCGGGCGCGCGCGGAGCGCCCCCGCGCGCGCGCC 360

QY 381 CCGCGCGCGCGCGCGCGCGCGCGCGCTCCATGACCGCTGATGGGGGTCAACAGCA 440
DB 361 CCGCGCGCGCGCGCGCGCGCGCGCGCTCCATGACCGCTGATGGGGGTCAACAGCA 420

QY 441 CCGCGCGCGCGCGCGCGCGCGCGCGCTCCATGACCGCTGATGGGGGTCAACAGCA 500
DB 421 CCGCGCGCGCGCGCGCGCGCGCGCGCTCCATGACCGCTGATGGGGGTCAACAGCA 480

QY 501 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 560

Db 481 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 540
QY 561 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 620
Db 541 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 600
QY 621 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 680
Db 601 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 660
QY 681 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 740
Db 661 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 720
QY 741 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 800
Db 721 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 780
QY 801 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 860
Db 781 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 840
QY 861 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 920
Db 841 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 900
QY 921 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 980
Db 901 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 960
QY 981 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1040
Db 961 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1020
QY 1041 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1100
Db 1021 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1080
QY 1101 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1160
Db 1081 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1140
QY 1161 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1220
Db 1141 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1200
QY 1221 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1280
Db 1201 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1260
QY 1281 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1321
Db 1261 TGTTCAGAGCATGGAGATCAACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGG 1301

RESULT 3
ACC49552
ID ACC49552 standard; cDNA; 4839 BP.
XX ACC49552;
AC ACC49552;
XX
DT 01-JUL-2003 (first entry)
XX
DE Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.
XX
KW Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
KW cancer; gene; ss.
XX
OS Homo sapiens.
XX
FN WO2003024392-A2.
XX

XX	ADP65729;	Db	1	GGAAAGCTAGCGGACAGAGGCTCAGCCCCCGCGGACGCGCGCCCCCGCTGCGCAGCCCAATT	60
AC		QY	153	TTCCGAGACGCCACCCCGCGGCACTGCGCGAGCGCCCCCGCGGCTGCGCGAGGAGCGCGGG	212
XX	12-AUG-2004 (first entry)	Db	61	TTCCGAGACGCCACCCCGCGGCACTGCGCGAGCGCCCCCGGCTGCGCGAGGAGCGCGGG	120
XX	Human transmembrane, prostate androgen induced RNA (TMSPAI), DNA.	QY	213	GGGCGAGCGGAGCGCGGTCCTCCGCGCACTGAGCCCCCGCGGCGCCCCCGGGAATTGCGGC	272
XX	autoimmune disease; arthritis; gene expression analysis;	Db	121	GGGCGAGCGGAGCGCGGTCCTCCGCGCACTGAGCCCCCGCGGCGCCCCCGGGAATTGCGGC	180
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;	QY	273	GGCCGAGCGCGGAGCGCGGCGCGCTCCCCCGCGCGCGCGCTCTCGCATGCGCGGC	332
KW	antiarthritic; osteopathic; antigout; antinflammatory; dermatological;	Db	181	GACCCGAGCGCGGAGCGCGGCGCGCTCCCCCGCGCGCGCTCTCTCGCATGCGCGGC	240
KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;	QY	333	CCGAGCTCCGCGGCGCGCGGAGCGCCCCCGCGGCGCCCCCGAGCCCCCGCGCGCGC	392
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;	Db	241	CCGAGCTCCGCGGCGCGCGGAGCGCCCCCGCGGCGCCCCCGAGCCCCCGCGCGCGC	300
XX	immune; ds; human.	QY	393	GCGCGCGCGCGCGCGCTCCATGCAACCGTTGATGGGGGTCAACAGCACGCGCGCGCGC	452
OS	Homo sapiens.	Db	301	GCGCGCGCGCGCGCGCTCCATGCAACCGTTGATGGGGGTCAACAGCACGCGCGCGCGC	360
XX	WO2003072827-A1.	QY	453	CGCGCGGCGAGCGCGCATGTCTCTGCACTGCACTGCAAACTCTTTGTTCCAGAGCA	512
XX	04-SEP-2003.	Db	361	CGCGCGGCGAGCGCGCATGTCTCTGCACTGCACTGCAAACTCTTTGTTCCAGAGCA	420
XX	31-OCT-2002; 2002WO-US035433.	QY	513	TGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATCTGCTGGTGTGATGATGTTGA	572
XX	31-OCT-2001; 2001US-0336220P.	Db	421	TGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATCTGCTGGTGTGATGATGTTGA	480
XX	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.	QY	573	TGCTGTGTGATACGTGCTGCTGAGCCACTACAAGTGTCTGCACTGCTTCTTCA	632
XX	Hirsch R, Thorton SL;	Db	481	TGCTGTGTGATACGTGCTGCTGAGCCACTACAAGTGTCTGCACTGCTTCTTCA	540
XX	WPI: 2003-712740/57.	QY	633	GCGCGCACAGCGGCGGAGGAGAGAGTGCCTGTCTCTCAGAGAGTGCCTGTGC	692
XX	GENBANK; NM_020182.	Db	541	GCGCGCACAGCGGCGGAGGAGAGAGTGCCTGTCTCTCAGAGAGTGCCTGTGC	600
PT	Diagnosing and analyzing autoimmune disease using gene expression	QY	693	CCTCGGAGAGCACAGTGTGTCAGCAACGGAATCCAGAGCGGAGGTCTACGCCCCGCTC	752
PT	profiles and microarray technology, useful for diagnosing and treating	Db	601	CCTCGGAGAGCACAGTGTGTCAGCAACGGAATCCAGAGCGGAGGTCTACGCCCCGCTC	660
PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and	QY	753	GCGCCACCGACCGCTGCGCGCTGCGCGCTTTCGCCAGCGGAGCGCTTCCACCGTTC	812
PT	gout.	Db	661	GCGCCACCGACCGCTGCGCGCTGCGCGCTTTCGCCAGCGGAGCGCTTCCACCGTTC	720
XX	Disclosure; Page: 56pp; English.	QY	813	AGCCACCTATCCGTACCTGTCAGCAGAGATCGACTGCCACCCACCATCTCGTGTGAG	872
XX	The invention relates to a novel method for diagnosing and analysing	Db	721	AGCCACCTATCCGTACCTGTCAGCAGAGATCGACTGCCACCCACCATCTCGTGTGAG	780
XX	autoimmune disease or arthritides. The method comprises obtaining a	QY	873	ACGGGAGAGAGCGCGCCACCTACCGGGGCGCTGCGCGACCTCCAGCTTCGCGGACCGCGAGC	932
CC	patient sample containing mRNA. Analysing gene expression using the mRNA	Db	781	ACGGGAGAGAGCGCGCCACCTACCGGGGCGCTGCGCGACCTCCAGCTTCGCGGACCGCGAGC	840
CC	that results in a gene expression signature of the mRNA, and using that	QY	933	AGCAGCTGGAACCTGAAACCGGGAGTGGTGGCGGCGCGCTGCGCGACCCCAACAGAACTTCGACA	992
CC	gene expression signature to diagnose or analyse the autoimmune disease	Db	841	AGCAGCTGGAACCTGAAACCGGGAGTGGTGGCGGCGCGCTGCGCGACCCCAACAGAACTTCGACA	900
CC	or arthritides in the patient, where gene expression of at least 60% of	QY	993	GTGACTGTGATGATGTGCGAGCTGGGCGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCA	1052
CC	the genes correlates with that of the gene signature. The invention	Db	901	GTGACTGTGATGATGTGCGAGCTGGGCGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCA	960
CC	further comprises: a treatment of rheumatoid arthritis; identification of	QY	1053	TCAGCGCCACGTGCTACCGGCGCGCGCGATGAGAGGGGCGCGCGCGCGCGCGCGCGCGCA	1112
CC	genes for targeting in the treatment of rheumatoid arthritis in a mammal	Db	961	TCAGCGCCACGTGCTACCGGCGCGCGCGATGAGAGGGGCGCGCGCGCGCGCGCGCGCGCA	1020
CC	other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an	QY	1113	AGGTATCGGCGCACTACCGGGGCTCTCTTCCAGCACAGAGAGAGTGGGCGCGCGCT	1172
CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or	Db	1021	AGGTATCGGCGCACTACCGGGGCTCTCTTCCAGCACAGAGAGAGTGGGCGCGCGCT	1080
CC	analyses of autoimmune disease or rheumatoid arthritis; screening the	QY	1173	CCTTGTGAGGGGACCGGGCTCCACCAACACATCGCGCGCGCTTAGAGAGCGAGCA	1232
CC	efficacy of a candidate drug in vitro for the treatment of collagen-	Db	1081	CCTTGTGAGGGGACCGGGCTCCACCAACACATCGCGCGCGCTTAGAGAGCGAGCA	1140
CC	induced arthritis; and reducing the symptoms associated with collagen-				
CC	induced arthritis. The compositions of the invention have the following				
CC	activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,				
CC	antigout, antinflammatory, dermatological, and immunomodulatory. The				
CC	methods and compositions of the present invention are useful for				
CC	diagnosing and treating autoimmune disease or arthritides, such as				
CC	rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,				
CC	fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an				
CC	immune disease caused by an infectious agent. This polynucleotide				
CC	represents a DNA sequence relating to the genes used in the analysis and				
CC	treatment of autoimmune diseases or arthritides. Note: This sequence is				
CC	not shown in the specification. It has been supplied in an electronic				
CC	format from WIPO.				
XX	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;				
XX	Query Match 93.0%; Score 1229; DB 11; Length 4839;				
XX	Best Local Similarity 100.0%; Pred. No. 6.4e-184;				
XX	Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	93 GGAAAGCTAGCGGACAGAGGCTCAGCCCCCGCGGAGCGCGCCCCCGCTGCGCAGCCCAATT				152

QY 1233 TCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGGCC 1292
DB 1141 TCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGGCC 1200
QY 1293 GGGCTGGGGCTGCTAGGTGAAAGGCAG 1321
DB 1201 GGGCTGGGGCTGCTAGGTGAAAGGCAG 1229

RESULT 6

ADM67045

ID ADM67045 standard; DNA; 4839 BP.

AC ADM67045;

XX 03-JUN-2004 (first entry)

XX Human homologue of murine adipocyte specific DNA SeqID 180.

KW human; adipocyte specific; ds; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive.

XX Homo sapiens.

OS WO2004011618-A2.

PN 05-FEB-2004.

PD 29-JUL-2003; 2003WO-US023684.

XX 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

XX (HMG-E-) HMG-E INC.

PA Chada K, Chouinard R, Ashar H, Sayed AMD;

XX WPI; 2004-143846/14.

DR Identifying adipocyte specific genes, useful for treating obesity or
XX diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.

XX Claim 11; SEQ ID NO 180; 91pp; English.

XX This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polynucleotide sequence is a human homologue
CC of a murine adipocyte specific DNA sequence of the invention.

SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match

Best Local Similarity 93.0%; Score 1229; DB 12; Length 4839;

Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTTAGCGGCAAGAGGCTCAGCCCCCGGCGGAGCGGCGCGCGCGCGCGCATTT 152
DB 1 GGAAGCTTAGCGGCAAGAGGCTCAGCCCCCGGCGGAGCGGCGCGCGCGCGCGCATTT 60
QY 153 TTCCGAGAGCCACCGCGGGGCACTGCGGACGCCCCCGGGGCTGCGGAGGGAGCGCGGG 212
DB 61 TTCCGAGAGCCACCGCGGGGCACTGCGGAGCGCCCCCGGGGCTGCGGAGGGAGCGCGGG 120
QY 213 GGGCGAGCGGAGCGGCTCCCGCGCACTGAGCCCCCGCGCGCGCGCGCGGAACTTGGCGG 272
DB 121 GGGCGAGCGGAGCGGCTCCCGCGCACTGAGCCCCCGCGCGCGCGCGGAACTTGGCGG 180
QY 273 GAGCGAGCGCGGAGCGCGGGCGGCGCTCCCGCGCGCGCGCGCGCGCTCTGTCATGCGGGG 332
DB 181 GAGCGAGCGCGGAGCGCGGGCGGCGCTCCCGCGCGCGCGCGCGCTCTGTCATGCGGGG 240
QY 333 CCAGCTCCGGGCGCGCGGAGCGCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
DB 241 CCAGCTCCGGGCGCGCGGAGCGCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 393 GCGCGCGCGCGCGCGCGCTCCATGCAACCGCTTGTATGGGGTCAACAGCAGCGCGCGCGCG 452
DB 301 GCGCGCGCGCGCGCGCTCCATGCAACCGCTTGTATGGGGTCAACAGCAGCGCGCGCGCG 360
QY 453 CCGCGGGGAGCGCCCAATGCTCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 512
DB 361 CCGCGGGGAGCGCCCAATGCTCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCA 420
QY 513 TGGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATCATCATCATCATCATCATCAT 572
DB 421 TGGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATCATCATCATCATCATCATCAT 480
QY 573 TGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 632
DB 481 TGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 633 GCGCGCAAGCGGCGGAGGAGAGAGATGCTCTCTCAGAGAGAGATGCTCTCTCAGAGAG 692
DB 541 GCGCGCAAGCGGCGGAGGAGAGAGATGCTCTCTCAGAGAGAGATGCTCTCTCAGAGAG 600
QY 693 CCTCGGAGGACAGTGTCTCAGCAAGGAATCCCGAGCGCGGAGGCTCTCAGCGCGCGCTC 752
DB 601 CCTCGGAGGACAGTGTCTCAGCAAGGAATCCCGAGCGCGGAGGCTCTCAGCGCGCGCTC 660
QY 753 GCGCCACCGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCG 812
DB 661 GCGCCACCGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCGCGCTGGCG 720
QY 813 AGCCACCTATCCGTACTGTCAGCAGAGATGAGCTGTCACCCACCATCTCGCTGTCTAG 872
DB 721 AGCCACCTATCCGTACTGTCAGCAGAGATGAGCTGTCACCCACCATCTCGCTGTCTAG 780
QY 873 AGGGGAGGAGCG 932
DB 781 AGGGGAGGAGCG 840
QY 933 AGCAGCTGGAATCTGAACCGGGAGTGGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCG 992
DB 841 AGCAGCTGGAATCTGAACCGGGAGTGGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCG 900
QY 993 GTGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
DB 901 GTGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 1053 TCAGCGCCAGCTGTCTACGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1112
DB 961 TCAGCGCCAGCTGTCTACGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1113 AGGTCTATCGGCCACTACCGGGGTCTCTCTTCCAGCACAGCAGAGAGAGTGGCGCGCGCT 1172
DB 1021 AGGTCTATCGGCCACTACCGGGGTCTCTCTTCCAGCACAGCAGAGAGAGTGGCGCGCGCT 1080

QY 633 GCCGCGACAGCCAGCGGCGGAGAGAGAAATCCCTGTCTCTCAGAAAGATGCTGTGGC 692
Db 541 GCCGCGACAGCCAGCGGCGGAGAGAGAAATCCCTGTCTCTCAGAAAGATGCTGTGGC 600
QY 693 CTTCCGAGAGACAGTGTCTAGGCAACGGATCCAGAGCGGAGGTCTAGCCCGCCCTC 752
Db 601 CTTCCGAGAGACAGTGTCTAGGCAACGGATCCAGAGCGGAGGTCTAGCCCGCCCTC 660
QY 753 GGCCACACCGACCGCTTGGCGGTGCGCCCTTCCGCCAGGCGGAGCGCTTCCACCGTTCC 812
Db 661 GGCCACACCGACCGCTTGGCGGTGCGCCCTTCCGCCAGGCGGAGCGCTTCCACCGTTCC 720
QY 813 AGCCACCTATCCGTACTGTCAGCAGCAGATGACCTGCCACCCACCATCTCTGTCAG 872
Db 721 AGCCACCTATCCGTACTGTCAGCAGCAGATGACCTGCCACCCACCATCTCTGTCAG 780
QY 873 AGGGGAGAGGCCCCACCTTACAGGCGGCGCCCTGCAACCTTCCAGCTTCGGGACCCCGAGC 932
Db 781 AGGGGAGAGGCCCCACCTTACAGGCGGCGCCCTGCAACCTTCCAGCTTCGGGACCCCGAGC 840
QY 933 AGCAGCTGGAACCTGAACCGGGAGTCTGTCGCGCACCCCAACAGAACCATCTTCGACA 992
Db 841 AGCAGCTGGAACCTGAACCGGGAGTCTGTCGCGCACCCCAACAGAACCATCTTCGACA 900
QY 993 GTGACCTGATGATGATGTCAGGCTGGGCGGCGCCCTTGCACCCCGCCAGCACTAATCGGGCA 1052
Db 901 GTGACCTGATGATGATGTCAGGCTGGGCGGCGCCCTTGCACCCCGCCAGCACTAATCGGGCA 960
QY 1053 TCAGCGCCACGCTGTCAGCGGCGGCGGCGGCGATGAGAGGCGCGCCGCCACCTACAGCG 1112
Db 961 TCAGCGCCACGCTGTCAGCGGCGGCGGCGGCGATGAGAGGCGCGCGCCGCCACCTACAGCG 1020
QY 1113 AGGTCTATCGGCACACTACCGGGGTCTCTTCCAGCACAGCAGAGCAGTGGCGCCCT 1172
Db 1021 AGGTCTATCGGCACACTACCGGGGTCTCTTCCAGCACAGCAGAGCAGTGGCGCCCT 1080
QY 1173 CTTGTGTAGAGGGGACCCGGCTCCACCAACACATCGCGCCCTTAGAGAGCGCAGCCA 1232
Db 1081 CTTGTGTAGAGGGGACCCGGCTCCACCAACACATCGCGCCCTTAGAGAGCGCAGCCA 1140
QY 1233 TCTGGAGCAAGAGAGGATTAACGAAAGGACACCCCTCTTAGGTCTCCAGGGGGGCC 1292
Db 1141 TCTGGAGCAAGAGAGGATTAACGAAAGGACACCCCTCTTAGGTCTCCAGGGGGGCC 1200
QY 1293 GGGCTGGGCTGCTAGGTGAAAGGCAG 1321
Db 1201 GGGCTGGGCTGCTAGGTGAAAGGCAG 1229

RESULT 9

ID ADC37326
X AC ADC37326 standard; DNA; 1383 BP.
X AC ADC37326;
X DT 18-DEC-2003 (first entry)
X DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 159.
X KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
X KW cancer; infectious disease; bone disease; AIDS;
X KW neurodegenerative disease; ischemic disorder; Antiinflammatory;
X KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
X KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
X OS Homo sapiens.
X PN WO2003048202-A2.
X PD 12-JUN-2003.
X PF 03-DEC-2002; 2002WO-JP012644.

PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX (ASAH) ASahi KASBI KK.
XX Matsuda A, Muramatsu S;
PI WPI; 2003-505282/47.
DR P-PSDB; ADC37327.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
PS Claim 4; SEQ ID NO 159; 938pp; English.
XX
CC The present invention relates to novel proteins and their coding
CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischemic disorders.
XX
SQ Sequence 1383 BP; 253 A; 505 C; 440 G; 185 T; 0 U; 0 Other;

Query Match 92.9%; Score 1227.4; DB 10; Length 1383;
Best Local Similarity 99.9%; Pred. No. 1.2e-183;
Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 93 GGAAGAGCTAGCGGAGAGGCTCAGCCCGCGGCGAGCGCGCGCTGCCAGGCCCAT 152
Db 1 GGAAGAGCTAGCGGAGAGGCTCAGCCCGCGGCGAGCGCGCGCTGCCAGGCCCAT 60
QY 153 TTCGAGAGCCACCGCGGCGACTGCGGACGCCCCCGGGGCTGCGGAGGGAGCGGGG 212
Db 61 TTCGAGAGCCACCGCGGCGACTGCGGACGCCCCCGGGGCTGCGGAGGGAGCGGGG 120
QY 213 GGGCGAGGAGCGGGTCCCGGCACTGAGCCCGCGGCGCGCGCGCGGAACTTGGCGGC 272
Db 121 GGGCGAGGAGCGGGTCCCGGCACTGAGCCCGCGGCGCGCGCGCGGAACTTGGCGGC 180
QY 273 GACCGAGCGCGGAGCGGGCGCGCTCCCGCGCGCGCGCGCTCTCTGATGCGGGGC 332
Db 181 GACCGAGCGCGGAGCGGGCGCGCTCCCGCGCGCGCGCGCTCTCTGATGCGGGGC 240
QY 333 CCCAGCTCGGGCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
Db 241 CCCAGCTCGGGCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 393 GCGCGCGCGCGCGCGGCTCATGCAACGGTTCATGGGGTCAACAGCACCGCGCGCGCG 452
Db 301 GCGCGCGCGCGCGCGGCTCATGCAACGGTTCATGGGGTCAACAGCACCGCGCGCGCG 360
QY 453 CGCGCGGAGCGGCAATGCTCTCAGTCACTGCAAAAGCTCTTGTTCAGAGCA 512
Db 361 CGCGCGGAGCGGCAATGCTCTCAGTCACTGCAAAAGCTCTTGTTCAGAGCA 420
QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCTGTTGGTGTGATGTTGA 572
Db 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCTGTTGGTGTGATGTTGA 480
QY 573 TGGTGGTGGTATCAGTGCCTCTGAGCCACTAAGCTGTCTGACGGTCTTCTATCA 632
Db 481 TGGTGGTGGTATCAGTGCCTCTGAGCCACTAAGCTGTCTGACGGTCTTCTATCA 540
QY 633 GCGCGCACAGCGGCGGAGGAGAGAGTGCCTCTCTCAGAAAGATCCCTGTGGC 692
Db 541 GCGCGCACAGCGGCGGAGGAGAGAGTGCCTCTCTCAGAAAGATCCCTGTGGC 600
QY 693 CTTGGAGAGCAGAGTGTTCAGGCAACGGAAATCCAGAGCGCGCAGGTCTACGCCGCTC 752


```
Db 601 CCTCGGAGACACAGTGTGAGGCAACGGAATCCAGAGCCGAGGTTACGCCCGCCCTC 660
Qy 753 GGCCCAACCGACCGCTTGGCGGTGCGCCCTTGCCTCCAGCGGAGCGCTTCCACCGTTCC 812
Db 661 GGCCCAACCGACCGCTTGGCGGTGCGCCCTTGCCTCCAGCGGAGCGCTTCCACCGTTCC 720
Qy 813 AGCCCAACCTTCCGTACCTGCAGCAGCAGAGATCGACCTGCCACCCACCATCTCGCTGTCAG 872
Db 721 AGCCCAACCTTCCGTACCTGCAGCAGCAGAGATCGACCTGCCACCCACCATCTCGCTGTCAG 780
Qy 873 ACGGAGAGAGCCGCCACCTTACAGGGCCCTTGCACCTTCCAGCTTTCGGGACCCCGAGC 932
Db 781 ACGGAGAGAGCCGCCACCTTACAGGGCCCTTGCACCTTCCAGCTTTCGGGACCCCGAGC 840
Qy 933 AGCAGCTGGAACCTGAACCGGGAGTCCGTGCGCGCACCCCAACAGAACCATCTTCGACA 992
Db 841 AGCAGCTGGAACCTGAACCGGGAGTCCGTGCGCGCACCCCAACAGAACCATCTTCGACA 900
Qy 993 GTGACCTGATGATAGTGCAGAGCTGGGGCGGCCCTTGCCTCCAGCAGGATTAACCTCGGGCA 1052
Db 901 GTGACCTGATGATAGTGCAGAGCTGGGGCGGCCCTTGCCTCCAGCAGGATTAACCTCGGGCA 960
Qy 1053 TCAGCGCCAGCTGTCTAGCGGAGCGGGCGCATGAGGGGGCGCGCCACCTACAGCG 1112
Db 961 TCAGCGCCAGCTGTCTAGCGGAGCGGGCGCATGAGGGGGCGCGCCACCTACAGCG 1020
Qy 1113 AGTCTATCGGCCACTACTCCCGGGTCTCTCTCCAGCAGCAGAGAGTGGCGGCCCT 1172
Db 1021 AGTCTATCGGCCACTACTCCCGGGTCTCTCTCCAGCAGCAGAGAGTGGCGGCCCT 1080
Qy 1173 CTTTGTGAGGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA 1232
Db 1081 CTTTGTGAGGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA 1140
Qy 1233 TCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGCTTCCCGGGGGCC 1292
Db 1141 TCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGCTTCCCGGGGGCC 1200
Qy 1293 GGCTCGGGCTGCTAGGTGAAAGGCAG 1321
Db 1201 GGCTCGGGCTGCTAGGTGAAAGGCAG 1229

RESULT 10
ADN38809
ID ADN38809 standard; cDNA; 864 BP.
XX AC ADN38809;
XX DT 17-JUN-2004 (first entry)
XX DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:127.
XX KW Human, differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX OS Homo sapiens.
XX PN WO2003042661-A2.
XX PD 22-MAY-2003.
XX PF 13-NOV-2002; 2002WO-US036810.
XX PR 13-NOV-2001; 2001US-0350666P.
XX PR 21-NOV-2001; 2001US-0332464P.
XX PR 29-NOV-2001; 2001US-0334393P.
```

```
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397752P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX PA Afar D, Ariz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
XX PI Mack DH, Murray R, Watson SR, Wilson KB, Zlotnik A;
XX DR WPI; 2003-468649/44.
XX DR P-PSDB; ADN38810.
XX CC Determining the presence or absence of a pathological cell in a patient,
XX PT useful for diagnosing, prognosing or treating cancer, comprises detecting
XX PT a nucleic acid in a biological sample.
XX PS Claim 8; SEQ ID NO 127; 1385pp; English.
XX CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX CC whose expression is upregulated or downregulated in specific cancers or
XX CC other diseases such as angiogenic or fibrotic disorders, and to methods
XX CC of determining the presence or absence of a pathological cell in a
XX CC patient by detecting a nucleic acid at least 80% identical to those of
XX CC the invention or by detecting a polypeptide of the invention. The
XX CC invention also relates to expression vectors and host cells comprising a
XX CC nucleic acid of the invention; antibodies which specifically bind a
XX CC polypeptide of the invention; use of such antibodies for drug targeting;
XX CC and methods of screening for modulators of activity or expression of the
XX CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX CC antibodies and methods are useful for diagnosing, prognosing and treating
XX CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
XX CC neovascularisation syndromes, scarring and uterine fibroids. They may
XX CC also be useful in wound healing and in contraception. The present
XX CC sequence represents a nucleic acid sequence of the invention.
XX SQ Sequence 864 BP; 173 A; 307 C; 254 G; 130 T; 0 U; 0 Other;
```

```
Query Match 65.4%; Score 864; DB 11; Length 864;
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 413 ATGCACCGTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCAATGTC 472
Db 1 ATGCACCGTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCAATGTC 60
Qy 473 TCTGTGACCTGCAACTGCAACGCTCTTTGTTCCAGAGCATGAGATCAGGAGCTGGAG 532
Db 61 TCTGTGACCTGCAACTGCAACGCTCTTTGTTCCAGAGCATGAGATCAGGAGCTGGAG 120
Qy 533 TTTGTTTCAGATCATCATCATCGTGGTGGTGCATGATGTTGTTGTTGATCAGTGC 592
Db 121 TTTGTTTCAGATCATCATCATCGTGGTGGTGCATGATGTTGTTGTTGATCAGTGC 180
Qy 593 CTGCTGAGCCACTACAAGCTGTGCA CGGTCTTTCATCAGCGCGCACAGCCAGGGCGG 652
Db 181 CTGCTGAGCCACTACAAGCTGTGCA CGGTCTTTCATCAGCGCGCACAGCCAGGGCGG 240
Qy 653 AGGAGAGAGATGCCCTGTCTCTCAGAGGATGCCTGTGCGCTCGGAGGACAGTGTCA 712
Db 241 AGGAGAGAGATGCCCTGTCTCTCAGAGGATGCCTGTGCGCTCGGAGGACAGTGTCA 300
```



```
QY 713 GGCAACGGAATCCAGAGCGCGAGGTCTACGCCCGCTCGGCCACCGACCGCTGGCC 772
Db 301 GGCAACGGAATCCAGAGCGCGAGGTCTACGCCCGCTCGGCCACCGACCGCTGGCC 360
QY 773 GTGCGCGCTTCGCCAGCGGAGCGCTTCACGCTTCAGGCCACCTATCGTACTG 832
Db 361 GTGCGCGCTTCGCCAGCGGAGCGCTTCACGCTTCAGGCCACCTATCGTACTG 420
QY 833 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTCAGACGGGAGGCCCCACCC 892
Db 421 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTCAGACGGGAGGCCCCACCC 480
QY 893 TACCAGGGCCCTTCACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCGG 952
Db 481 TACCAGGGCCCTTCACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCGG 540
QY 953 GAGTCGGTGGCGGACCCCAACAGAACCATCTTCGACGATGATGATGATGATG 1012
Db 541 GAGTCGGTGGCGGACCCCAACAGAACCATCTTCGACGATGATGATGATGATG 600
QY 1013 AGGCTGGGGCGCCCTGCGCCCGCCAGCAGTAATCTCGGGCATCAGCGCTACGGC 1072
Db 601 AGGCTGGGGCGCCCTGCGCCCGCCAGCAGTAATCTCGGGCATCAGCGCTACGGC 660
QY 1073 AGCGGGCGCGCATGGAGGGCGCGCGCCACCTACAGCGAGGTCTATCGGCCACTACCGG 1132
Db 661 AGCGGGCGCGCATGGAGGGCGCGCGCCACCTACAGCGAGGTCTATCGGCCACTACCGG 720
QY 1133 GGGTCTCTCTTCAGCAGCAGCAGAGAGTGGCGCGCCCTCTTGTGAGGGGACCGG 1192
Db 721 GGGTCTCTCTTCAGCAGCAGCAGAGAGTGGCGCGCCCTCTTGTGAGGGGACCGG 780
QY 1193 CTCACACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 1252
Db 781 CTCACACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 840
QY 1253 AAACAGAAAGGACACCTCTCTTAG 1276
Db 841 AAACAGAAAGGACACCTCTCTTAG 864

RESULT 11
AAA75151
ID AAA75151 standard; cDNA; 969 BP.
XX
AC AAA75151,
XX
DE 15-JAN-2001 (first entry)
XX
DE cDNA encoding a human TANGO 261 polypeptide.
XX
KW TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
KW cellular proliferation; cellular differentiation; cellular adhesion;
KW von Willebrand factor-associated disorder; cell trafficking; cancer;
KW hematopoietic associated disease; atelectasis; pulmonary congestion;
KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
KW intestinal disorder; spleen associated disease; renal disorder;
KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
KW brain herniation; iatrogenic disease; inflammation; meningitis;
KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 6..764
XX /*tag= a
XX /product= "TANGO 261"
XX sig_peptide 6..89
XX /*tag= b
XX mat_peptide 90..764
XX /*tag= c
```

```
XX WO200052022-A1.
PN
XX
PD 08-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US005226.
XX
PR 01-MAR-1999; 99US-0122458P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX
XX WPI; 2000-579269/54.
DR P-PSDB; AAB18449.
XX
XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
PT treating cancer.
XX
XX Claim 2; Fig 5; 175pp; English.
XX
XX The present sequence encodes a human TANGO 261 polypeptide. The
CC specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
CC 267. The TANGO polypeptides can be used to modulate cellular
CC proliferation, modulate cellular differentiation and/or modulate cellular
CC adhesion. The proteins can be used to treat any von Willebrand factor-
CC associated disorder, regulate extracellular matrix structuring, cellular
CC adhesion, and cell trafficking and/or migration, modulate cellular
CC interactions, modulate cell adhesion in proliferative disorders, such as
CC cancer, modulate the proliferation, differentiation, and/or function of
CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
CC blood and hematopoietic associated diseases and disorders, atelectasis,
CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
CC asthma and bronchiectasis, intestinal disorders, spleen associated
CC diseases, modulate renal disorders, treat cardiovascular disorders such
CC as ischemic heart disease, modulate the proliferation, differentiation,
CC and/or function of bone and cartilage cells and to treat bone and/or
CC cartilage associated diseases or disorder. They may also be used to treat
CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
CC disease, multiple sclerosis, brain cancers, hydrocephalus and
CC encephalitis, and treat hepatic disorders
XX
XX Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;
QY 514 GCAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGTGGTGGTGGTGGT 573
Db 2 GGAGATGGCGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGTGGTGGTGGTGGT 61
QY 574 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 633
Db 62 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121
QY 634 CCGGACAGCCAGGGGGCGGAGAGAGATGCCCTGTCTCAGAGAGATGCTGTGGGCC 693
Db 122 CCGGACAGCCAGGGGGCGGAGAGAGATGCCCTGTCTCAGAGAGATGCTGTGGGCC 181
QY 694 CTCGGAGAGCAGGTGTCTAGGCAACGGATCCAGAGCGCGAGGTCTACGCCCGCTCG 753
Db 182 CTCGGAGAGCAGGTGTCTAGGCAACGGATCCAGAGCGCGAGGTCTACGCCCGCTCG 241
QY 754 GCCCACCGACCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 813
Db 242 GCCCACCGACCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 301
QY 814 GCCCACCTATCCGTACCTGTCAGCAGCAGATCGACCTGCCACCCACCATCTCGTGTCA 873
```

Query Match 60.8%; Score 803.2; DB 3; Length 969;
Best Local Similarity 99.6%; Pred. No. 3.8e-117;
Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 302 GCCACCTATCCGTACCTGACGACGAGATCGACCTGCGGCCACCATCTCGTGTGAGA 361
QY 874 CGGGAGAGCCCCACCTTACAGAGCCCTGACCCCTCCAGCTTGGGACCCGAGCA 933
Db 362 CGGGAGAGCCCCACCTTACAGAGCCCTGACCCCTCCAGCTTGGGACCCGAGCA 421
QY 934 GCAGCTGGAATCAACCGGAGTGGTGGCGGCACCCCAACCAACATCTTCGACG 993
Db 422 GCAGCTGGAATCAACCGGAGTGGTGGCGGCACCCCAACCAACATCTTCGACG 481
QY 994 TGACCTGATGATAGTGCAGGCTGGGCGGCCCTTGGCCCCCAGCAGTAACCTCGGCAT 1053
Db 482 TGACCTGATGATAGTGCAGGCTGGGCGGCCCTTGGCCCCCAGCAGTAACCTCGGCAT 541
QY 1054 CAGCGCCACCTGTACGGCAGCGCGCGGCATGAGGGGCCCGCCCACTTACAGCGA 1113
Db 542 CAGCGCCACCTGTACGGCAGCGCGCGGCATGAGGGGCCCGCCCACTTACAGCGA 601
QY 1114 GGTCTCGGCACATACCCGGGTCTCTTCCAGCACCAGCAGAGTGGCGGCCCTC 1173
Db 602 GGTCTCGGCACATACCCGGGTCTCTTCCAGCACCAGCAGAGTGGCGGCCCTC 661
QY 1174 CTTGCTGGAGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCAT 1233
Db 662 CTTGCTGGAGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCAT 721
QY 1234 CTGGAGCAAGAGAGATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGCGG 1293
Db 722 CTGGAGCAAGAGAGATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGCGG 781
QY 1294 GGCTGGGGCTGCTAGGTGAAAGGCGAG 1321
Db 782 GGCTGGGGCTGCTAGGTGAAAGGCGAG 809

RESULT 12
ABK92120
ID ABK92120 standard; DNA; 1140 BP.
XX
AC ABK92120;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #6.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX Mammalia.
OS
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288569P.
XX
(BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI; 2002-471335/50.
DR P-PSDB; ABG61805.

XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 305; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridize to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 U; 0 Other;
Query Match 60.7%; Score 802.2; DB 6; Length 1140;
Best Local Similarity 98.4%; Pred. No. 5.4e-117;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 499 TTTGTTCCAGAGCATCGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCTCGTGT 558
Db 77 TCTCTCGCAAAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCTCGTGT 136
QY 559 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
Db 137 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
QY 619 ACGGTCTTTCATCAGCGCGGCACAGCCAGGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 678
Db 197 ACGGTCTTTCATCAGCGCGGCACAGCCAGGGCGGAGAGAGAGAGAGAGAGAGAGAG 256
QY 679 AGGATGCTGTGGCCCTCGGAGAGACAGTGTGAGCAACGGAATCCAGAGCGCAGGT 738
Db 257 AGGATGCTGTGGCCCTCGGAGAGACAGTGTGAGCAACGGAATCCAGAGCGCAGGT 316
QY 739 CTAGCGCCCGCTCGGCGCCACCGACCGCTGGCGCTGGCGCCCTTGGCCAGCGGGAGCG 798
Db 317 CTAGCGCCCGCTCGGCGCCACCGACCGCTGGCGCTGGCGCCCTTGGCCAGCGGGAGCG 376
QY 799 CTTCCACCGCTTCCAGCCCACTTATCCGTACCTGACGACGAGATGACCTGACCCAC 858
Db 377 CTTCCACCGCTTCCAGCCCACTTATCCGTACCTGACGACGAGATGACCTGACCCAC 436
QY 859 CATCTCGTGTACAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
Db 437 CATCTCGTGTACAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 496
QY 919 TCGGGAACCGGAGCAGAGCTGGAACCTGAACCGGGAGTGGTGGCGGACCCCAACAG 978
Db 497 TCGGGAACCGGAGCAGAGCTGGAACCTGAACCGGGAGTGGTGGCGGACCCCAACAG 556
QY 979 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1038
Db 557 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 616
QY 1039 CAGTAACCTCGGGCATCAGGCGCACTGCTACGCGAGCGCGGCGCATGAGAGGGCGGCC 1098
Db 617 CAGTAACCTCGGGCATCAGGCGCACTGCTACGCGAGCGCGGCGCATGAGAGGGCGGCC 676
QY 1099 GCCACCTACAGGAGGTGATCGGCCACTACCGGGGTCTCTTCTTCAGCAGCAGCAGAG 1158
|||||

Db 677 GCCCACCCTACAGCGAGGTTCATCGGCCACTACCGCGGGTCTCTCCAGCACCAGCAGAG 736
QY 1159 CAGTGGGCGCGCCCTCTCTGCTGGAGGGACCCGGCTCCACCACACACACATCGCGCCCT 1218
Db 737 CAGTGGGCGCGCCCTCTCTGCTGGAGGGACCCGGCTCCACCACACACACATCGCGCCCT 796
QY 1219 AGAGAGCGCAGCCATCTGGAGCAAGAGAGAGATAAACAGAAAGGACACCCCTCTCTAGGG 1278
Db 797 AGAGAGCGCAGCCATCTGGAGCAAGAGAGAGATAAACAGAAAGGACACCCCTCTCTAGGG 856
QY 1279 TCCCCAGGGGCGCGGCTGGGGCTGGCTAGGTGAAAGGCGAG 1321
Db 857 TCCCCAGGGGCGCGGCTGGGGCTGGCTAGGTGAAAGGCGAG 899

RESULT 13

ADB75588

ID ADB75588 standard; cDNA; 1141 BP.

AC ADB75588;

XX 04-DEC-2003 (first entry)

XX Prostate cancer marker cDNA.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Homo sapiens.

XX WO2003009814-A2.

XX 06-FEB-2003.

XX 25-JUL-2002; 2002WO-US023913.

XX 25-JUL-2001; 2001US-0307982P.

XX 22-AUG-2001; 2001US-0314356P.

XX 25-SEP-2001; 2001US-0325020P.

XX 12-DEC-2001; 2001US-0341746P.

XX 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

XX Hoerhn S, Kamatkar S, Monsey AM, Glatt K, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

XX cancer.

XX Disclosure; SEQ ID NO 412; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1141 BP; 271 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

XX Query Match 60.7%; Score 802.2; DB 10; Length 1141;

XX Best Local Similarity 98.4%; Pred. No. 5.4e-117;

Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 499 TTGTTCAGAGATCGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTGTGT 558

Db 77 TCTCTCGCAAAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCTGTGT 136

QY 559 GGTGATGATGGTGATCGTGGTGATCAGCTGCCTCTGAGCCACTACAGCTGTCTCC 618

Db 137 GGTGATGATGGTGATCGTGGTGATCAGCTGCCTCTGAGCCACTACAGCTGTCTCC 196

QY 619 ACGTCTCTTTCATCAGCGGCACAGCCAGGGGCGGAGAGAGAGATGCCCTGTCTCTCAGA 678

Db 197 ACGTCTCTTTCATCAGCGGCACAGCCAGGGGCGGAGAGAGAGATGCCCTGTCTCTCAGA 256

QY 679 AGGATGCTGTGGCCCTCGGAGAGACAGTGTTCAGGCAACGGAATCCCAAGCGCGAGGT 738

Db 257 AGGATGCTGTGGCCCTCGGAGAGACAGTGTTCAGGCAACGGAATCCCAAGCGCGAGGT 316

QY 739 CTACGCCCGCCCTCGGCCACACCGCTGCGCGCTGCGCGCTTCCGCCAGCGGAGCG 798

Db 317 CTACGCCCGCCCTCGGCCACACCGCTGCGCGCTGCGCGCTTCCGCCAGCGGAGCG 376

QY 799 CTTTCCACCGCTTCCAGCCCACTATCCGTAACCTGACGACGAGATCGACTGCCACCCAC 858

Db 377 CTTTCCACCGCTTCCAGCCCACTATCCGTAACCTGACGACGAGATCGACTGCCACCCAC 436

QY 859 CATCTCGCTGTCAGACGGGAGGAGCCGCCACCTACCGAGGCGCCCTGACCTCCAGCT 918

Db 437 CATCTCGCTGTCAGACGGGAGGAGCCGCCACCTACCGAGGCGCCCTGACCTCCAGCT 496

QY 919 TCGGACCCCGGAGCAGCTGGAACCTGAACCGGAGTCCGTCGCGCAACCCCAACAG 978

Db 497 TCGGACCCCGGAGCAGCTGGAACCTGAACCGGAGTCCGTCGCGCAACCCCAACAG 556

QY 979 AACCATCTTCGACGACGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1038

Db 557 AACCATCTTCGACGACGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 616

QY 1039 CAGTAACTCGGGCATCAGCGCCACCTGCTAGGGCAGCGCGCGCATGGAGGGGCGCC 1098

Db 617 CAGTAACTCGGGCATCAGCGCCACCTGCTAGGGCAGCGCGCGCATGGAGGGGCGCC 676

QY 1099 GCGCACCTACAGCAGGTCATCGGCACCTACCGGGGTCCTCTTCAGACACCCAGAG 1158

Db 677 GCGCACCTACAGCAGGTCATCGGCACCTACCGGGGTCCTCTTCAGACACCCAGAG 736

QY 1159 CAGTGGGCGCGCCCTCTCTGCTGGAGGGACCGGGCTCCACACACACATCGCGCCCT 1218

Db 737 CAGTGGGCGCGCCCTCTCTGCTGGAGGGACCGGGCTCCACACACACATCGCGCCCT 796

QY 1219 AGAGAGCGCAGCCATCTCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278

Db 797 AGAGAGCGCAGCCATCTCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856

QY 1279 TCCCCAGGGGCGCGGCTGGGGCTGGCTAGGTGAGTGAAGAGGCGAG 1321

Db 857 TCCCCAGGGGCGCGGCTGGGGCTGGCTAGGTGAGTGAAGAGGCGAG 899

RESULT 14

ACC49536

ID ACC49536 standard; cDNA; 1850 BP.

XX ACC49536;

XX 01-JUL-2003 (first entry)

XX Tumour-associated antigenic target protein TAT180 cDNA SEQ ID NO:44.

XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;

XX cancer; gene; ss.

XX Homo sapiens.

treating prostate cancer or other prostatic pathologies, e.g. prostatitis.

Claim 9; SEQ ID NO 2; 43pp; English.

The invention relates to a substantially pure androgen responsive prostate specific (ARP) nucleic acid molecule selected from ARP1-ARPS (appearing as ADL83312, ADL83313, ADL83315, ADL83317 and ADL83319. Also included are methods of diagnosing or predicting susceptibility to a prostate neoplastic condition in an individual, methods for treating or reducing the severity of a prostate neoplastic condition in an individual, a substantially pure ARP3, ARP4 or ARPS polypeptide (or their fragments, encoded by the above ARP3, ARP4 or ARPS nucleic acid molecule, respectively) and a binding agent comprising a molecule that selectively binds the above ARP3, ARP4 or ARPS polypeptide. The nucleic acid molecules and polypeptides are useful in diagnosing, preventing and treating prostate cancer or other prostate pathologies such as benign prostatic hyperplasia or prostatitis. The nucleic acid molecules are used as hybridisation probes in various diagnostic procedures. The present sequence is the ARP2 cDNA.

XX
SQ Sequence 4527 BP; 1089 A; 1149 C; 1175 G; 1113 T; 0 U; 1 Other;

Query Match 60.7%; Score 802.2; DB 11; Length 4527;

Best Local Similarity 98.4%; Pred. No. 5e-117;

Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 499 TTGTTCCAGAGCATCGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCGTGGT 558
DB 77 TCTCTCGGNAACAGGCAATGGCGAGCTGGAGTTGTTTCAGATCATCATCGTGGT 136
QY 559 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
DB 137 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
QY 619 ACGGTCTTCATCAGCGGACAGCCAGCGGCGGAGAGAGAGATGCCCTGTCCTCAGA 678
DB 197 ACGGTCTTCATCAGCGGACAGCCAGCGGCGGAGAGAGATGCCCTGTCCTCAGA 256
QY 679 AGGATGCTGTGGCCCTCGGAGAGCAGTGTGATGATGATGATGATGATGATGATGAT 738
DB 257 AGGATGCTGTGGCCCTCGGAGAGCAGTGTGATGATGATGATGATGATGATGATGAT 316
QY 739 CTACGCCGCCCTCGGCCACCGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 798
DB 317 CTACGCCGCCCTCGGCCACCGCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 376
QY 799 CTTCCACCGCTTCAGCGGACCTATCGGTACCTGACGACGACGATCGACCTGCCACCCAC 858
DB 377 CTTCCACCGCTTCAGCGGACCTATCGGTACCTGACGACGACGATCGACCTGCCACCCAC 436
QY 859 CATCTCGCTGTACAGCGGAGAGCGCCCGCCCTACCGGGCCCTGCGACCCCTCCAGCT 918
DB 437 CATCTCGCTGTACAGCGGAGAGCGCCCGCCCTACCGGGCCCTGCGACCCCTCCAGCT 496
QY 919 TCGGGACCCCGACGACGCTGGAATGAACTGAACTGAACTGAACTGAACTGAACTGAA 978
DB 497 TCGGGACCCCGACGACGCTGGAATGAACTGAACTGAACTGAACTGAACTGAACTGAA 556
QY 979 AACCATCTTCGACAGTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1038
DB 557 AACCATCTTCGACAGTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 616
QY 1039 CAGTAACCTGGGATCAGCGGACGCTGCTACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1098
DB 617 CAGTAACCTGGGATCAGCGGACGCTGCTACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 676
QY 1099 GCCCACTTACGAGAGGTTCATCGGCCACTACCGGGGCTCTCTCTCCAGCACGACGAG 1158
DB 677 GCCCACTTACGAGAGGTTCATCGGCCACTACCGGGGCTCTCTCTCCAGCACGACGAG 736
QY 1159 CAGTGGGCGGCGGCT 1218

Db 737 CAGTGGGCGGCGGCT 796
QY 1219 AGAGAGCGCGAGCCATCTGGAGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTTAGGG 1278
Db 797 AGAGAGCGCGAGCCATCTGGAGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTCTTAGGG 856
QY 1279 TCCCCAGGGGGGCGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 1321
Db 857 TCCCCAGGGGGGCGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG 899

Search completed: February 19, 2005, 11:44:04
Job time : 712.116 secs


```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,952A
; FILING DATE: 19-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,278
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: PCT/US97/19381
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Timothy L.
; REGISTRATION NUMBER: 35,367
; REFERENCE/DOCKET NUMBER: 015280-297100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX: <Unknown>
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1...921
; OTHER INFORMATION: clone 22 coding region
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
;
US-09-091-952A-7
Query Match 26.7%; Score 352.2; DB 3; Length 921;
Best Local Similarity 73.1%; Pred. No. 1.3e-58;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 506 CAGAGCATGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTCGTGGTGGTATG 565
DB 166 CCGGGATCTTCACTCGGAGCTGGAGTTGCCCAATCATCATCTCGTGGTGGTGC 225
QY 566 ATGGTATGTTGGTGGTATGATCGTCTGCTGAGGCACTACAAAGTCTTCACAGGTC 625
DB 226 ACGGTATGTTGGTGGTATGATCGTCTGCTGAGGCACTACAAAGTCTTCACAGGTC 285
QY 626 TTATCGCCCGGACAGCCAGGCGGAGGAGAGAGATGCCCTGTCTCAGAGGATGC 695
DB 286 TTATCAACCGCCGAAACCAAGAGCCGAGGCGGAGGAGCGGCTGCCGCAAGGAGTGC 345
QY 686 CTGTGCGCTTCGAGAGCAGATGTTCAGGCAACGGAATCCAGAGCGGCAAGTCTACGCC 745
DB 346 CTGTGCGCTTCAGAGCGCGCCAGCCCGGCTGGG-----CGCTCGGAGATCATGCAT 399
QY 746 CCGCTTCGGCCCAACCGACCGCTGGCGGTGGCGCCCTTCGCCCGAGGGGAGCGCTTCCAC 805
DB 400 GCCCGCGGTCCAGGACAGGTTTCAGAGCGCGCTTCCTCATCAGAGGATCGCTTCAGC 459
QY 806 CGCTTCAGCCCACTATTCGTATCTGTCAGCAGAGATCGACCTGCCACCCACATCTCG 865
DB 460 CGCTTCAGCCCACTATTCGTATCTGTCAGCAGAGATTCATCTCTCCACCATCTCC 519
QY 866 CTGTGAGCGGGAGGAGCCCGACCTACAGGGCCCTGCACCTCCAGCTTCGGGAC 925
DB 520 CTGTCCGACGGTGAAGAGCCACTCTCTTACAGGGCCCTGACCTTCGAGCTCCGGGAC 579
QY 926 CCGAGCAGCAGCTGGAATCGAACCGGGAGTTCGGTCGCGCACCCCGCCCAAGAACCATC 985
DB 580 CTTGACAGCAGATGGAACTCAACCGAGTTCGTCGAGGCGCCCAACCCACCGAACCAT 639
QY 986 TTCGACAGTACCTGATGGATATGTCAGG---CTGGGCGGCGCCCTGTGCCCCCGCAGT 1042

;
;
; Db 640 TTTGACAGTATTATATACATTTGTATGTATAGCGGGGTCCATGCCCACCCAGCAGC 699
; QY 1043 AACTCGGGCATCAGCCCGTCTACGCGAGCGGGCGCGCATGAGAGGGCGCGCCGCC 1102
; Db 700 AACTCGGGCATCAGTCAAGACACCTGCAGCAGTAACGGGAGGATGAGAGGGGCCACCC 759
; QY 1103 ACCTACAGCGAGTCAATCGGCCACTACCCGGGTCTCTTCCAGCACCAGCAGCAG 1161
; Db 760 ACATACAGCGAGTGTATGGGCCACCCAGCGGCTCTTTCTTCATCACCAGCGGAG 818
;
;
; RESULT 4
; US-09-091-952A-6
; Sequence 6, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa B.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,952A
; FILING DATE: 19-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,278
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: PCT/US97/19381
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Timothy L.
; REGISTRATION NUMBER: 35,367
; REFERENCE/DOCKET NUMBER: 015280-297100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8065 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1...8065
; OTHER INFORMATION: Clone 22
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116...1036
; OTHER INFORMATION: Clone 22 coding region
; FEATURE:
```


CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...867
OTHER INFORMATION: Clone 22 isoform 2 alternatively
spliced coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-091-952A-8

Query Match 21.5%; Score 284.2; DB 3; Length 867;
Best Local Similarity 68.7%; Pred. No. 1.3e-45;
Matches 453; Conservative 0; Mismatches 143; Indels 63; Gaps 2;
QY 506 CAGAGATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTATG 565
DB 166 CCGGGCATCTTCAACTCGGAGCTGGAGTTCCGCCAAATCATCATCATCGTGGTGGT 225
QY 566 ATGTCATGGTGTGTGATCATCGTGCCTGCTGAGCCACTACAGTGTCTGCAAGTCC 625
DB 226 ACGGTGATGGTGTGTGTCATGCTGCTGCTGAAACCACTACAAAGTCTCCACGCGGTC 285
QY 626 TTTCATCAGCCGCGACACCGAGCGGCGGAGGAGAGATGCCCTGTCTCCTCAGAAGGATGC 685
DB 286 TTTCATCAACCGCCCGACACCGAGCGGCGGAGCGGAGCGGGCT----- 329
QY 686 CTGTGCCCCCTCGGAGAGCACAGTGTTCAGGCAACGGAAATCCAGAGCGCGAGTCTACGCC 745
DB 330 -----GCCGACATCATGTCAT 345
QY 746 CCGCCTCGGCCACCGACCGCCTGGCGGTGCGCCCTTCCGCCAGCGGGAGCGCCTCCAC 805
DB 346 GCCCGCGGTTCAGGGACAGAGTTTCACAGCGCGCTCTTCATCCAGAGGGATCGCTTCAGC 405
QY 806 CGCTTCAGCCCACTATCGTACCTGTCGACGAGATCGACCTGCCACCCACCATCTCG 865
DB 406 CGCTTCAGCCCACTATCGTACCTGTCGACGAGATGATCTTCTCCACCATCTCC 465
QY 866 CTGTACAGCGGGAGGAGGAGCGCCCTACAGGGCGCCCTGACCCCTCCAGCTTCGGGAC 925

DB 466 CTGTCCGCGGTGAAGAGCCACCTCTCTTACAGGGGCCCTGACCCCTGACGCTCCGGAC 525
QY 926 CCGAGCAGCAGCTGGAACCTGAACCGGGAGTCCGGTGGCGCACACCCCAACAGAACCATC 985
DB 526 CCGTGAACAGCAGATGGAACCTGAACCGAGTCCGTGAGGGCCCAACCAACCGAACCAT 585
QY 986 TTGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1042
DB 586 TTGACAGTGAATTAATAGACATTTGCTATGATATAGCGGGGGTTCATGCCCCCAGCAGC 645
QY 1043 AACTCGGGCATCAGCGCCAGCTGCTACGCGCGGGCGGCGATGGAGGGGGCGCGCGCC 1102
DB 646 AACTCGGGCATCAGTGAAGACCTGACAGCATTAACGGAGGATGAGGGGGCGCACCCCC 705
QY 1103 AACTCAGCGAGGTCTATCGGCCACTACCGGGGGTCTCTTCCAGCACCGAGAGCAG 1161
DB 706 ACATACAGCGAGGTGATGGGCCACCCAGCGGGCGCTCTTCTCCATCATCAGCGGCG 764
RESULT 7
US-09-621-976-2162
; Sequence 2162, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2162
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 17..223
US-09-621-976-2162
Query Match 6.8%; Score 90.4; DB 4; Length 391;
Best Local Similarity 75.7%; Pred. No. 1.5e-08;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1019 GCGGGCCCTGCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1078
DB 26 GCGGGTCCATGCCCCACCCAGCAGCAACTCGGGCATCATCGGCGGCGGCGGCGGCGGCG 85
QY 1079 GCGGCGCATGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1138
DB 86 GGAGAGATGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 145
QY 1139 TCCTTCCAGCACCGAGCAGCAGTGGGC 1166
DB 146 TCCTTCCATCATCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 173
RESULT 8
US-09-616-289-48/c
; Sequence 48, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001

Qy	98	GCTAGCGGAGAGGCTCAGCCCCCGCGCGGAGCGCGCGCCCGCTGCAGGCCCATTTTCG	157
Db	24175	GCGAGCCCCCGGAGCCCCCGCGAGCCCCCGGAGCCCCCGCGAGCCCCCGCG	24116
Qy	158	GACGCCACCCCGGGGCACTGCCGAGCGCCCGGGGCTGCCGAGGGGAGGCCGGGGGGCG	217
Db	24115	GAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAG	24056
Qy	218	CAGCGGAGCGGTCCTCCGCGACTGAGCCCGCGGGCGCCCGGGAACCTTGGCGCGCACCC	277
Db	24055	CCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCC	23996
Qy	278	GAGCCCGCGGAGCCGGGCGCGCTCCCGCGCGCGCGCTCTGTGATGGGGGCGCCCGAG	337
Db	23995	CCCCCGGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCC	23936
Qy	338	CTCCGGGCGCGCGGAGCCCCCGCGCGCGCCCCCGAGCCCCCGCGCCCCCGCGCGCGC	397
Db	23935	CCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAGCCCCCGCGAG	23876
Qy	398	GCGCGCGGCGGTCCTATGACCG	420
Db	23875	GCGAGCCCCCGCGCCCTGCACTG	23853

```

RESULT 11
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

```

Query Match	5.3%;	Score 70.4;	DB 3;	Length 4403765;
Best Local Similarity	50.0%;	Pred. No. 0.00046;		
Matches 230;	Conservative 0;	Mismatches 226;	Indels 4;	Gaps 2;
Qy	2	GACCGCGTCTCGAGCGAAACCCGATCTCCTTGGACTTGAACTGAGGAGGAGGAGCGCGC	61	
Db	3936335	GCCGCGGCGAACGCGGGCA	CCGCGCGGCAGAGCGCGGAGTGGTGGCGCGCGCGGCGACGGT	3936394
Qy	62	GGCGCGCGCGCGCGCGAGGCGCTCGGCTGGGGAAAGCTAGCGCGACAGAGCTTCAGCCCCG	121	
Db	3936395	ATCGTGGCGTTCGCGCGCGCAAGCGCGGCGCAACGCGCGGACGGCGAAGTCGCGCGTGC	3936454	
Qy	122	CGCGCAGGCGCGCGCGCGCTGCCAGCCCATTTTCGGACGCGCACCCCGCGGCATGCGC	- 180	
Db	3936455	GGCGCGCGCGCGCGACGCGGCGCCCAACACCAAGTCTCCGCGGCGCAACGCGCGGCAAGAGGT	3936514	
Qy	181	-ACGCCCCCGGGTTCGCGAGGCGAGGCGCGGGGGGGCGCAGCGAGGCGCGGTCCCGCGCA	239	
Db	3936515	CAAGCGGCACGGTGGTCCGCTGGGGCGGCGCGGGCTGGCGCGCGGGTGGGGGCGCT	3936574	
Qy	240	CTGAGCCCCCGCGCGCCCGGGAACTTGGGGGGAACCCGAGCCCGCGGACCGCGGGGCGCG	299	

[illegible][illegible]

RESULT 13
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328


```
Qy 169 CGGCACTGCGAGCCCGGGGCTGCCGAGGGGCGGGGGGCGAGCGAGCGC 228
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2003 CACACTGAGCTGAGCCCGACCGGACCGGGCTGGGCGCGGCGCTGTGTGGCG 1944
Qy 229 GGTCCCGCGCACTGAGCCCGCGCGCCCGGGAACTTGGCGGCGACCCGAGCCCGCGCGA 288
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1943 GCTGCTGCTGCGGTTACCATGGCAACCCCGGGCCCGCGCGCGCGAGCGCGCGA 1884
Qy 289 GCCGGGGCGCGCTTCCCGCGCGCGCGCTTCTGCAATGCGGGGCGCGAGCTCCGGGGCGC 348
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1883 GCCCAGCGCCCGCTCCGC--CCGCGAGGGGGCGCGCTCGGCGCGCGGGGCCCGGGCCG 1826
Qy 349 GCGCGGAGCCCCCGGGCGCGCCCGAGCGCCCGGGCGCGCGCGCGCGCGCGCGCGCC 408
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1825 GGAGGGGGACGTGGCGGGGCGGGCGAGCTCCCGCGCTTGGGCGCTTTTCCCGCG 1766
Qy 409 GTCCATGCAACCGCTTGATGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCA 468
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1765 GGGAGCGCGGCGCGGGCGGCTGGGAGCCGAGGGGGCGGTCTGCGCGCGCGCTGTCCCT 1706
Qy 469 TGTC 472
Db | | |
1705 TGGC 1702
```

Search completed: February 19, 2005, 16:22:50
Job time : 260.374 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 14:21:20 ; Search time 742.23 Seconds
(without alignments)
10519.334 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccggtctcgagcgca.....ctgcgtagtgaaagcgag 1321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10769316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1321	100.0	1321	9 US-09-934-249-1	Sequence 1, Appli
2	1229	93.0	4839	15 US-10-241-220-119	Sequence 119, App
3	1229	93.0	4839	16 US-10-269-909-84	Sequence 84, Appl
4	1229	93.0	4839	16 US-10-269-909-85	Sequence 85, Appl
5	1229	93.0	4839	18 US-10-872-972-119	Sequence 119, App
6	1229	93.0	4839	18 US-10-872-991-119	Sequence 119, App
7	864	65.4	864	17 US-10-295-027-127	Sequence 127, App
8	861	65.2	861	9 US-09-934-249-3	Sequence 3, Appli
9	803.2	60.8	969	10 US-09-796-753-55	Sequence 55, Appl
10	802.2	60.7	1141	15 US-10-205-823-412	Sequence 412, App
11	802.2	60.7	1141	15 US-10-301-822-208	Sequence 208, App

12	802.2	60.7	1850	15	US-10-241-220-44	Sequence 44, Appl
13	802.2	60.7	1850	18	US-10-872-972-44	Sequence 44, Appl
14	802.2	60.7	1850	18	US-10-872-991-44	Sequence 44, Appl
15	802.2	60.7	4527	10	US-09-821-812-2	Sequence 2, Appli
16	802.2	60.7	4527	18	US-10-849-635-2	Sequence 2, Appli
17	801.6	60.7	1140	16	US-10-390-045-1	Sequence 1, Appli
18	801.6	60.7	1140	17	US-10-434-479-1	Sequence 1, Appli
19	790.4	59.8	1066	13	US-10-098-841-71	Sequence 71, Appl
20	767.4	58.1	806	15	US-10-241-220-45	Sequence 45, Appl
21	767.4	58.1	806	18	US-10-872-972-45	Sequence 45, Appl
22	767.4	58.1	806	18	US-10-872-991-45	Sequence 45, Appl
23	755.8	57.2	759	16	US-10-390-045-2	Sequence 2, Appli
24	755.8	57.2	759	17	US-10-434-479-2	Sequence 2, Appli
25	616.4	46.7	878	9	US-09-934-249-12	Sequence 12, Appl
26	589.2	44.6	1583	14	US-10-000-256A-32	Sequence 32, Appl
27	493.6	37.4	693	9	US-09-934-249-14	Sequence 14, Appl
28	466.2	35.3	1713	10	US-09-796-753-57	Sequence 57, Appl
29	352.2	26.7	921	16	US-10-251-598-7	Sequence 0, Appli
30	352.2	26.7	8018	13	US-10-087-192-1667	Sequence 1667, Ap
31	352.2	26.7	8065	16	US-10-251-598-6	Sequence 0, Appli
32	350	26.5	920	9	US-09-823-245A-20	Sequence 20, Appl
33	350	26.5	2170	17	US-10-094-749-197	Sequence 197, App
34	349	26.4	8093	9	US-09-934-249-16	Sequence 16, Appl
35	349	26.4	8093	17	US-10-172-118-1023	Sequence 1023, Ap
36	349	26.4	8093	17	US-10-342-887-1023	Sequence 1023, Ap
37	341.8	25.9	475	9	US-09-934-249-15	Sequence 15, Appl
38	298	22.6	837	18	US-10-363-345A-30089	Sequence 30089, A
39	298	22.6	837	18	US-10-363-345A-30090	Sequence 30090, A
40	284.2	21.5	867	16	US-10-251-598-8	Sequence 0, Appli
41	270.8	20.5	837	18	US-10-363-345A-30091	Sequence 30091, A
42	270.8	20.5	837	18	US-10-363-345A-30092	Sequence 30092, A
43	250.2	18.9	285020	13	US-10-087-192-1666	Sequence 1666, Ap
44	182	13.8	368	9	US-09-783-590-3464	Sequence 3464, Ap
45	182	13.8	467	10	US-09-918-995-2074	Sequence 2074, Ap

ALIGNMENTS

RESULT 1

US-09-934-249-1
; Sequence 1, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John F.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934, 249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (413)...(1273)
US-09-934-249-1

Query Match 100.0%; Score 1321; DB 9; Length 1321;
Best Local Similarity 100.0%; Pred. No. 2.8e-310;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCGGCTCTCGAGCGCAACCCGATCTCTTGACTTGATGAGGAGGAGCGG 60

Db 1 CGAGCGGGTCTCGAGCGGAAACCCGATCTCTTTGGACTTGAATAGGAGGAGAGGCGG 60
Qy 61 CGGCGCGCGCGCGCGAGCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120
Db 61 CGGCGCGCGCGCGCGAGCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120
Qy 121 GCGGAGAGCGCGCGCGCGCTGCGAGCCCAATTTTCGAGCGCCACCGCGGGGCACTGCGG 180
Db 121 GCGGAGAGCGCGCGCGCGCTGCGAGCCCAATTTTCGAGCGCCACCGCGGGCACTGCGG 180
Qy 181 ACCGCGCGGGTTCGAGGAGGAGCGCGGGGGGCGCAGCGAGCGCGTCCGCGCAC 240
Db 181 ACCGCGCGGGTTCGAGGAGGAGCGCGGGGGGCGCAGCGAGCGCGTCCGCGCAC 240
Qy 241 TGAGCGCGCGCGCGCGCGGAACTTGGCGGCGACCGCGCGGCGAGCGCGGGCGCG 300
Db 241 TGAGCGCGCGCGCGCGCGGAACTTGGCGGCGACCGCGCGGCGAGCGCGGGCGCG 300
Qy 301 CTCGCGCGCGCGCGCTCTGATGCGGGGCGCCAGCTCCGGGCGCGCGCGAGCGCC 360
Db 301 CTCGCGCGCGCGCGCTCTGATGCGGGGCGCCAGCTCCGGGCGCGCGCGAGCGCC 360
Qy 361 CCGGCGCGCGCGAGCG 420
Db 361 CCGGCGCGCGCGAGCG 420
Qy 421 CTTGATGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 421 CTTGATGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 481 GTGCAACTGCAACCGCTTTTGTTCAGAGCATGGAGATCAGCGAGCTGGAGTTGTCA 540
Db 481 GTGCAACTGCAACCGCTTTTGTTCAGAGCATGGAGATCAGCGAGCTGGAGTTGTCA 540
Qy 541 GATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 541 GATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
Qy 601 CCACTACAAGCTGTCTGACGCTCTTTCATCAGCGCGCAGCAGCGGGGCGAGGAGA 660
Db 601 CCACTACAAGCTGTCTGACGCTCTTTCATCAGCGCGCAGCAGCGGGGCGAGGAGA 660
Qy 661 AGATGCGCTCTCTGAGAGATGCTGCTGCGGCTCGGAGACACAGTGTACGCAACGG 720
Db 661 AGATGCGCTCTCTGAGAGATGCTGCTGCGGCTCGGAGACACAGTGTACGCAACGG 720
Qy 721 AATCCAGAGCGCGAGTGTACGCGCGCGCTCGGCGCAGCAGCGCGCTGCGCGCG 780
Db 721 AATCCAGAGCGCGAGTGTACGCGCGCGCTCGGCGCAGCAGCGCGCTGCGCGCG 780
Qy 781 CTTGCGCGCGGAGCGCTTCCAGCGCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 781 CTTGCGCGCGGAGCGCTTCCAGCGCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCG 840
Qy 841 GATCGACCTTCCACCACTCTCGTGTGAGCGGGAGGCGCGCGCGCGCGCGCGCG 900
Db 841 GATCGACCTTCCACCACTCTCGTGTGAGCGGGAGGCGCGCGCGCGCGCGCGCG 900
Qy 901 CCCTGCACTCTGAGCTTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 901 CCCTGCACTCTGAGCTTGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Qy 961 GCGCGCACCCCAACAGAACCTTTCGAGAGTGAAGCTGATGATGATGATGATGATG 1020
Db 961 GCGCGCACCCCAACAGAACCTTTCGAGAGTGAAGCTGATGATGATGATGATGATG 1020
Qy 1021 CGGCG 1080
Db 1021 CGGCG 1080
Qy 1081 GCGATGAGGAGCG 1140
Db 1081 GCGATGAGGAGCG 1140

Qy 1141 CTTCCAGCACCGAGCAGAGCAGTGGGCGCGCTCTCTTGTGGAGGGAACCGGCTCCACCA 1200
Db 1141 CTTCCAGCACCGAGCAGAGCAGTGGGCGCGCTCTCTTGTGGAGGGAACCGGCTCCACCA 1200
Qy 1201 CACACATCATGCGCGCGCTAGAGAGCGCAGCATCTGGAGCAAGAGATAAACAGAA 1260
Db 1201 CACACATCATGCGCGCGCTAGAGAGCGCAGCATCTGGAGCAAGAGATAAACAGAA 1260
Qy 1261 AGGACACCTCTCTAGGGTCCCAGGGGGCGGGCTGGGGTGCCTAGGTGAAAAGGCA 1320
Db 1261 AGGACACCTCTCTAGGGTCCCAGGGGGCGGGCTGGGGTGCCTAGGTGAAAAGGCA 1320
Qy 1321 G 1321
Db 1321 G 1321

RESULT 2
US-10-241-220-119
; Sequence 119, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-119

Query Match 93.0%; Score 1229; DB 15; Length 4839;
Best Local Similarity 100.0%; Pred. No. 5,7e-288;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAGCTAGCGGAGAGGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 152
Db 1 GGAAGCTAGCGGAGAGGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Qy 153 TTCCGAGCG 212
Db 61 TTCCGAGCG 120
Qy 213 GCGCGAGCGGAGCG 272
Db 121 GCGCGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 273 GACCGAGCG 332
Db 181 GACCGAGCG 240
Qy 333 CCAGCTCCGGGCG 392
Db 241 CCAGCTCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy 393 GCG 452
Db 301 GCG 360
Qy 453 CCGCGCGGAGCG 512

QY	153	TTCCGAGACGCCACCCGCGGGGCACTGCGAGCGCCGCCCGGGGCTGCGGAGGGGAGGCGCGGG	213
Db			
QY	61	TTCCGAGACGCCACCCGCGGGGCACTGCGGAGCGCCGCCCGGGGCTGCGGAGGGGAGGCGCGGG	120
Db			
QY	213	GGGCGGACGGAGCGCGGTCCCGGGCACTGAGCCCCCGGGCGGCCCGGGAATCTTGGCGGC	272
Db			
QY	121	GGGCGGACGGAGCGCGGTCCCGGGCACTGAGAGCCCCCGGGCGGCCCGGGAATCTTGGCGGC	180
Db			
QY	273	GACCCGAGCCCGGGGAGCCGGGGCGCGCTCCCCCGCGCGCGCGCTCTCTGCAATCGGGGC	332
Db			
QY	181	GACCCGAGCCCGGGGAGCCGGGGCGCGCTCCCCCGCGCGCGCGCTCTCTGCAATGGGGGC	240
Db			
QY	333	CCCAGCTCCGGGCGCGCGCGCGGAGCCCCCGCGCGCGCCCCCGAGCCCCCGCGCGCGCGC	392
Db			
QY	241	CCCAGCTCCGGGCGCGCGCGGAGCCCCCGCGCGCGCGCCCCCGAGCCCCCGCGCGCGCGC	300
Db			
QY	393	GCCGGCGCGCGCGCGCGCTCATGCAACCGCTTGATGGGGGTCAAAGACACCGCGCGCGCGC	452
Db			
QY	301	GCCGGCGCGCGCGCGCGCTCATGCAACCGCTTGATGGGGGTCAAAGACACCGCGCGCGCGC	360
Db			
QY	453	CCGCGGGGAGCCAACTGTCTCTGCAAGTGCACCTGCAAAAGCTCTTTGTTCCAGAGCA	512
Db			
QY	361	CCGCGGGGAGCCAACTGTCTCTGCAAGTGCACCTGCAAAAGCTCTTTGTTCCAGAGCA	420
Db			
QY	513	TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGTGATGTGTA	572
Db			
QY	421	TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGTGATGTGTA	480
Db			
QY	573	TGGTGGTGGTATCACGTGCCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTTCATCA	632
Db			
QY	481	TGSGTGGTGTATCACGTGCCCTGCTGAGCCACTAAAGCTGTCTGCAAGGCTCTTCATCA	540
Db			
QY	633	GCCGGCACAGCCAGGGCGGAGGAGAGAAGATGCCCTGTCTCTCAGAAAGGATGCCTGTGGC	692
Db			
QY	541	GCCGGCACAGCCAGGGCGGAGGAGAGAAGATGCCCTGTCTCTCAGAAAGGATGCCTGTGGC	600
Db			
QY	693	CCTCGGAGAGCACAGTGTTCAGGCAACGGAAATCCAGAGCCGCAAGTCTACGCCCGCGCTC	752
Db			
QY	601	CCTCGGAGAGCACAGTGTTCAGGCAACGGAAATCCAGAGCCGCAAGTCTACGCCCGCGCTC	660
Db			
QY	753	GGCCGACGACCGCTGGCGGTGGCGCCCTTGCGCCGAGCGGGAGGCTTCAACCGCTTCC	812
Db			
QY	661	GGCCGACGACCGCTGGCGGTGGCGCCCTTGCGCCGAGCGGGAGCGCTTCCACCGCTTCC	720
Db			
QY	813	AGCCACCTATCTCGTACTGTCAGCACAGAGATCGACCTGCCACCCACCATCTCTCGTGTCA	872
Db			
QY	721	AGCCACCTATCTCGTACTGTCAGCACAGAGATCGACCTGCCACCCACCATCTCTCGTGTCA	780
Db			
QY	873	ACGGGAGGAGCCCCCAACCTTACAGGGCCCCCTGCACCCCTCCAGTCTGGGACCCCGAGC	932
Db			
QY	781	ACGGGAGGAGCCCCCAACCTTACAGGGCCCCCTGCACCCCTCCAGTCTGGGACCCCGAGC	840
Db			
QY	933	AGCAGCTGGAACTGAAACGGGAGTGGTGGCGCACCCCGCAACAGAAACATCTTTCAGCA	992
Db			
QY	841	AGCAGCTGGAACTGAAACGGGAGTGGTGGCGCACCCCGCAACAGAAACATCTTTCAGCA	900
Db			
QY	993	GTGACCTCATGATAGTGCAGGCTGGCGCGCCCTGCCCGCCAGCAGTAACTCTCGGCA	1052
Db			
QY	901	GTGACCTCATGATAGTGCAGGCTGGCGCGCCCTGCCCGCCAGCAGTAACTCTCGGCA	960
Db			
QY	1053	TCAGCGCACCGTGTATAGGCAAGCGCGCGCGCATGAGGGGCGCGCCACCTACACGCG	1112
Db			
QY	961	TCAGCGCACCGTGTATAGGCAAGCGCGCGCGCATGAGGGGCGCGCCACCTACACGCG	1020
Db			
QY	1113	AGGTATATCGGCCCATACCCCGGGGTCTCTCTTTCAGCAACAGCAGCAGTGGGCGCGCCT	1172
Db			
QY	1021	AGGTATATCGGCCCATACCCCGGGGTCTCTCTTTCAGCAACAGCAGCAGTGGGCGCGCCT	1080
Db			
QY	1173	CCTTGTCTGGAGGACCGCGCTCCACCAACACATCTCGGCCCTTAGAGAGCGCAGCCA	1232
Db			
QY	1081	CCTTGTCTGGAGGACCGCGCTCCACCAACACATCTCGGCCCTTAGAGAGCGCAGCCA	1140
Db			
QY	1233	TCTGGAGCAAGAGAAAGATAAACAGAAAGGACACCTCTCTAGGGGTCCCCCAGGGGGGCC	1292

RESULT 7

```

US-10-295-027-127
; Sequence 127, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynné, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIORITY APPLICATION NUMBER: US 09/663,733
; PRIORITY FILING DATE: 2000-09-15
; PRIORITY APPLICATION NUMBER: US 60/350,666
; PRIORITY FILING DATE: 2001-11-13
; PRIORITY APPLICATION NUMBER: US 60/335,394
; PRIORITY FILING DATE: 2001-11-15
; PRIORITY APPLICATION NUMBER: US 60/332,464
; PRIORITY FILING DATE: 2001-11-21
; PRIORITY APPLICATION NUMBER: US 60/334,393
; PRIORITY FILING DATE: 2001-11-29
; PRIORITY APPLICATION NUMBER: US 60/340,376
; PRIORITY FILING DATE: 2001-12-14
; PRIORITY APPLICATION NUMBER: US 60/347,211
; PRIORITY FILING DATE: 2002-01-08
; PRIORITY APPLICATION NUMBER: US 60/347,349
; PRIORITY FILING DATE: 2002-01-10
; PRIORITY APPLICATION NUMBER: US 60/355,250
; PRIORITY FILING DATE: 2002-02-08
; PRIORITY APPLICATION NUMBER: US 60/356,714
; PRIORITY FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-127

```

	Query Match	65.4%;	Score 864;	DB 17;	Length 864;	
	Best Local Similarity	100.0%;	Pred. No. 1.3e-199;			
	Matches 864;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	413	ATGCACCGCTTCATGGGGGTCAACAGCACGCGCGCCGCCGCGGGCAGCCCATGTC	472			
Dd	1	ATGCACCGCTTCATGGGGGTCAACAGCACGCGCGCCGCCGCGGGCAGCCCATGTC	60			
Qy	473	TCTGTGCACGTGCAACTGCAAAACGCTCTTTTGTTCAGAGCATGGAGATCACGGAGCTGGAG	532			
Dd	61	TCTGTGCACGTGCAACTGCAAAACGCTCTTTTGTTCAGAGCATGGAGATCACGGAGCTGGAG	120			
Qy	533	TTTGTTTCAGATCATCATCATCTCGTGTGTGTATGATGGTGATGGTGATCATCGTGC	592			
Dd	121	TTTGTTTCAGATCATCATCTCGTGTGTGTATGATGGTGATGGTGATCATCGTGC	180			

QY 593 CTGCTGAGCCACTACAGCTGTCTGCAAGTCTCTTATCAGCGGCGCACAGCCAGGGCGG 652
Db 181 CTGCTGAGCCACTACAGCTGTCTGCAAGTCTCTTATCAGCGGCGCACAGCCAGGGCGG 240
QY 653 AGGAGAGAGATGCTCTGCTCAGAGAGATGCTGTGGCCCTCGAGAGACACAGTGTCA 712
Db 241 AGGAGAGAGATGCTCTGCTCAGAGAGATGCTGTGGCCCTCGAGAGACACAGTGTCA 300
QY 713 GGCAACGGAATCCAGAGCGCGAGTGTACGCCGCCGCTCGGCCCAACCGACCGCTGGCC 772
Db 301 GGCAACGGAATCCAGAGCGCGAGTGTACGCCGCCGCTCGGCCCAACCGACCGCTGGCC 360
QY 773 GTGCGGCCCTTCGCCCGAGCGGAGCGCTTCCAGCGCTTCAGGCCCACTTCCGTACTG 832
Db 361 GTGCGGCCCTTCGCCCGAGCGGAGCGCTTCCAGCGCTTCAGGCCCACTTCCGTACTG 420
QY 833 CAGCAGAGATCGACTGCGCCACCCACCATCTCGCTGTGACAGCGGAGAGCGCCACCC 892
Db 421 CAGCAGAGATCGACTGCGCCACCCACCATCTCGCTGTGACAGCGGAGAGCGCCACCC 480
QY 893 TACCAGGGCCCTTCGACCCCTTCCAGCTTCGGGACCCCGAGCAGCTGGAACTGAAACCGG 952
Db 481 TACCAGGGCCCTTCGACCCCTTCCAGCTTCGGGACCCCGAGCAGCTGGAACTGAAACCGG 540
QY 953 GAGTGGTGGCGGCGACCCCAACAGAACCATCTTGCAGTGCACCTGATGGATGTGCC 1012
Db 541 GAGTGGTGGCGGCGACCCCAACAGAACCATCTTGCAGTGCACCTGATGGATGTGCC 600
QY 1013 AGGCTGGGGCGCCCTTCGCCCGCCCGCCAGCACTTCCGGGATCAGCGCCAGCTGACGGC 1072
Db 601 AGGCTGGGGCGCCCTTCGCCCGCCCGCCAGCACTTCCGGGATCAGCGCCAGCTGACGGC 660
QY 1073 AGCGGGGGCGCATGAGGGGGCGCGCCCACTTACAGCGAGTCTATCGGCCACTACCCCG 1132
Db 661 AGCGGGGGCGCATGAGGGGGCGCGCCCACTTACAGCGAGTCTATCGGCCACTACCCCG 720
QY 1133 GGGTCTCTCTTCAGCAGCAGCAGAGAGAGTGGCGCGCTCTTCTGCTGGAGGGGACCCGG 1192
Db 721 GGGTCTCTCTTCAGCAGCAGCAGAGAGAGTGGCGCGCTCTTCTGCTGGAGGGGACCCGG 780
QY 1193 CTCACACACACACATCGCGCCCTTAGAGAGCGAGCCATCTGGAGCGAAAGAGAGGAT 1252
Db 781 CTCACACACACACATCGCGCCCTTAGAGAGCGAGCCATCTGGAGCGAAAGAGAGGAT 840
QY 1253 AAACAGAAAGGACACCCCTCTCTAG 1276
Db 841 AAACAGAAAGGACACCCCTCTCTAG 864

RESULT 8

US-09-934-249-3
; Sequence 3, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John P.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934,249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 3
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1)... (861)
US-09-934-249-3
Query Match 65.2%; Score 861; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 7,1e-199; Indels 0; Gaps 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 413 ATGCAACCGCTTGTATGGGGGTCAACAGCACCGCGCGCCCGCGCGGAGCCCAATGTC 472
Db 1 ATGCAACCGCTTGTATGGGGGTCAACAGCACCGCGCGCGCGCGGAGCCCAATGTC 60
QY 473 TCTGCACTGCAACTGCAAAAGCTCTTTGTTCCAGAGCATGAGAGATCAGGAGCTGGAG 532
Db 61 TCTGCACTGCAACTGCAAAAGCTCTTTGTTCCAGAGCATGAGAGATCAGGAGCTGGAG 120
QY 533 TTTGTTTCAGATCATCATCATCGTGGTGGTGTATGATGATGATGATGATGATGATGATG 592
Db 121 TTTGTTTCAGATCATCATCATCGTGGTGGTGTATGATGATGATGATGATGATGATGATG 180
QY 593 CTGCTGAGCCACTTACAAGCTGTCTGCAAGCTCTTCTTATCAGCGGCGCACAGCCAGGGCGG 652
Db 181 CTGCTGAGCCACTTACAAGCTGTCTGCAAGCTCTTCTTATCAGCGGCGCACAGCCAGGGCGG 240
QY 653 AGGAGAGAGATGCGCTGTCTTCTCAGAGAGATGCTGTGGCCCTTCGGAGAGCAGTGTCA 712
Db 241 AGGAGAGAGATGCGCTGTCTTCTCAGAGAGATGCTGTGGCCCTTCGGAGAGCAGTGTCA 300
QY 713 GGCAACGGAATCCAGAGCGCGAGTGTACGCCGCCGCTCGGCCCAACCGACCGCTGGCC 772
Db 301 GGCAACGGAATCCAGAGCGCGAGTGTACGCCGCCGCTCGGCCCAACCGACCGCTGGCC 360
QY 773 GTGCGGCCCTTCGCCCGAGCGGAGCGCTTCCACCGCTTCCAGCGCCACTATCCGTACTG 832
Db 361 GTGCGGCCCTTCGCCCGAGCGGAGCGCTTCCACCGCTTCCAGCGCCACTATCCGTACTG 420
QY 833 CAGCAGAGATGCACTGTGCAACCCACCATCTCTGCTGTGAGAGGGAGAGCCCGACCC 892
Db 421 CAGCAGAGATGCACTGTGCAACCCACCATCTCTGCTGTGAGAGGGAGAGCCCGACCC 480
QY 893 TACCAGGGCCCTTCGACCCCTTCCAGCTTCGGGACCCCGAGCAGCTGGAACTGAAACCGG 952
Db 481 TACCAGGGCCCTTCGACCCCTTCCAGCTTCGGGACCCCGAGCAGCTGGAACTGAAACCGG 540
QY 953 GAGTGGTGGCGGCGACCCCAACAGAACCATCTTGCAGAGTGCACCTGATGGATGTGCC 1012
Db 541 GAGTGGTGGCGGCGACCCCAACAGAACCATCTTGCAGAGTGCACCTGATGGATGTGCC 600
QY 1013 AGGCTGGGGCGCCCTTCGCCCGCCCGCCAGCACTTCCGGGATCAGCGCCAGCTGCTAGCGG 1072
Db 601 AGGCTGGGGCGCCCTTCGCCCGCCCGCCAGCACTTCCGGGATCAGCGCCAGCTGCTAGCGG 660
QY 1073 AGCGGGGGCGCATGAGGGGGCGCGCCCACTTACAGCGAGTCTATCGGCCACTACCCCG 1132
Db 661 AGCGGGGGCGCATGAGGGGGCGCGCCCACTTACAGCGAGTCTATCGGCCACTACCCCG 720
QY 1133 GGGTCTCTCTTCCAGCAGCAGCAGAGTGGCGCGCTCTTCTGCTGGAGGGGAGCCCGG 1192
Db 721 GGGTCTCTCTTCCAGCAGCAGCAGAGTGGCGCGCTCTTCTGCTGGAGGGGAGCCCGG 780
QY 1193 CTCACACACACACATCGCGCCCTTAGAGAGCGGAGCCATCTGGAGCGAAAGAGAGGAT 1252
Db 781 CTCACACACACACATCGCGCCCTTAGAGAGCGGAGCCATCTGGAGCGAAAGAGAGGAT 840
QY 1253 AAACAGAAAGGACACCCCTCTC 1273
Db 841 AAACAGAAAGGACACCCCTCTC 861

RESULT 9

US-09-796-753-55
; Sequence 55, Application US/09796753
; Publication No. US20030027998A1

; GENERAL INFORMATION:
 ; APPLICANT: McCarthy, Sean A.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 :
 : FILE REFERENCE: 7853-227-999
 :
 : CURRENT APPLICATION NUMBER: US/09/796,753

; CURRENT APPLICATION NUMBER: US/09/796,753
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 09/183,175

; PRIOR APPLICATION NUMBER: 09/183,175
 ;
 ; PRIOR FILING DATE: 1998-10-30
 ;
 ; PRIOR APPLICATION NUMBER: 09/223,094

; PRIOR APPLICATION NUMBER: 09/223,094
 ;
 ; PRIOR FILING DATE: 1998-12-30
 ;
 ; PRIOR APPLICATION NUMBER: 09/223,546

; PRIOR APPLICATION NUMBER: 09/223,546
 ;
 ; PRIOR FILING DATE: 1998-12-30
 ;
 ; PRIOR APPLICATION NUMBER: 09/224,246

; PRIOR APPLICATION NUMBER: 09/224,246
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/259,388

; PRIOR APPLICATION NUMBER: 09/259,388
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/122,458

; PRIOR APPLICATION NUMBER: 60/122,458
 ; PRIOR FILING DATE: 1999-03-01
 ; PRIOR APPLICATION NUMBER: 09/312,359

; PRIOR APPLICATION NUMBER: 09/312,359
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 09/336,536

; PRIOR APPLICATION NUMBER: 09/336,536
 ; PRIOR FILING DATE: 1999-06-18
 ; PRIOR APPLICATION NUMBER: 09/342,687

; PRIOR APPLICATION NUMBER: 09/342,687
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 09/345,464

; PRIOR APPLICATION NUMBER: 09/345,464
 ; PRIOR FILING DATE: 1999-06-30
 ; PRIOR APPLICATION NUMBER: 09/365,164

;
;
;
;
;

; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634

; PRIOR APPLICATION NUMBER: 09/409,634
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: 09/471,179

; PRIOR APPLICATION NUMBER: 09/471,179
 ;
 ; PRIOR FILING DATE: 1999-12-23
 ;
 ; PRIOR APPLICATION NUMBER: 09/474,071
 ;

; PRIOR APPLICATION NUMBER: 09/474,071
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/474,072

; PRIOR APPLICATION NUMBER: 09/474,072
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/514,010

; PRIOR APPLICATION NUMBER: 09/514,010
 ;
 ; PRIOR FILING DATE: 2000-02-25
 ;
 ; PRIOR APPLICATION NUMBER: 09/516,745
 ;

Db	2	GGAGATGGCGGAGCTGGAGTTTGTTCAGATCATCATCTGTTGGTGGTATGATGGTGTAT	61
Qy	574	GGTGGTGGTGTATCAGTTCSCCTGCTGAGCCACTACAAGCTGTCTGCAGGTCCTTTCATCAG	633
Db	62	GGTGGTGGTGTATCAGTTCSCCTGCTGAGCCACTACAAGCTGTCTGCAGGTCCTTTCATCAG	121
Qy	634	CCGGCACAACCCAGGGGGCGAGAGAGAAGATGCCCTGTCTCAGAAGGATGCCTGTGGCC	693
Db	122	CCGGCACAACCCAGGGGGCGAGAGAGAAGATGCCCTGTCTCAGAAGGATGCCTGTGGCC	181
Qy	694	CTGGAGAGCAAGTGTTCAGCAACCGGAATCCAGAGCCGAGGTCCTACGCCGCCGCCCTCG	753
Db	182	CTGGAGAGCAAGTGTTCAGCAACCGGAATCCAGAGCCGAGGTCCTACGCCGCCGCCCTCG	241
Qy	754	GCCCAACGACCCGCTGGCCGCTGCGCCCTTCGCCCAGCGGGAGCGCTTCACCGGTTCCA	813
Db	242	GCCCAACGACCCGCTGGCCGCTGCGCCCTTCGCCCAGCGGGAGCGCTTCACCGGTTCCA	301
Qy	814	GCCCACTATCCGTACTCTGCAGCAGCAGATGCGACTGCGCACCCACCACTCTCGCTGTGAGA	873
Db	302	GCCCACTATCCGTACTCTGCAGCAGCAGATGCGACTGCGCGCCACCACTCTCGCTGTGAGA	361
Qy	874	CGGGAGGAGCCCCCACTACAGGGCCCTTGCAACCTTCAGCTTCGGGACCCCGAGCA	933
Db	362	CGGGAGGAGCCCCCACTACAGGGCCCTTGCAACCTTCAGCTTCGGGACCCCGAGCA	421
Qy	934	GCAGCTGGAACTGAACCCGGGAGTTCGGTGGGGGACACCCCAACAGAACCACTTCTCGACAG	993
Db	422	GCAGCTGGAACTGAACCCGGGAGTTCGGTGGGGGACACCCCAACAGAACCACTTCTCGACAG	481
Qy	994	TGACCTGATGTAGTGCAGGCTGGCGGCCCTTGCCCCCAGCAGTAGTAACCTCGGCGCAT	1053
Db	482	TGACCTGATGTAGTGCAGGCTGGCGGCCCTTGCCCCCAGCAGTAGTAACCTCGGCGCAT	541
Qy	1054	CAGCGCCAAGTGTACGGCAGCGCGGGCGCATGGAGGGGCGCGGCCCACTACAGCGA	1113
Db	542	CAGCGCCAAGTGTACGGCAGCGCGGGCGCATGGAGGGGCGCGGCCCACTACAGCGA	601
Qy	1114	GGTCATCGGCCACTACCCGGGCTCTCTTCAGCACACGAGCAGTAGTGGGCGCGCCCTC	1173
Db	602	GGTCATCGGCCACTACCCGGGCTCTCTTCAGCACACGAGCAGTAGTGGGCGCGCCCTC	661
Qy	1174	CTTGCTGGAGGGGACCCGGTTCACACACACATCGCCCTCAGAGAGCGAGCGCAT	1233
Db	662	CTTGCTGGAGGGGACCCGGTTCACACACACATCGCCCTCAGAGAGCGAGCGCAT	721
Qy	1234	CTGAGCAAAAGAGAGGATAAACAAGAGACACCTCTCTTAGGGTCCCAAGGGGGCCG	1293
Db	722	CTGAGCAAAAGAGAGGATAAACAAGAGACACCTCTCTTAGGGTCCCAAGGGGGCCG	781
Qy	1294	GGCTGGGGCTGCTAGTGTGAAAAGGCGAG	1321
Db	782	GGCTGGGGCTGCTAGTGTGAAAAGGCGAG	809

RESULT 10

US-10-205-823-412

; Sequence 412, Application US/10205823

; Publication No. US20030108963A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E

; APPLICANT: Endege, Wilson

; APPLICANT: Gannavarapu, Manjula

APPLICANT: Gorbacheva, Bella
APPLICANT: Gorbacheva, Bella
APPLICANT: Gorbacheva, Bella

APPLICANT: Hoersch, Sebastian
APPLICANT: Karmatkar, Shubhanshi

```

; APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Wensev Angel a M

```

; APPLICANT: Wonsey, Angela M.
: APPLICANT: Glatz Karen

APPLICANT: Zhao, Xumei

```

; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin

```

APPLICANT: ALDEISON, DUSTIN
TITLE OF INVENTION: NOVEL GENES.

THE TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TILE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 412
LENGTH: 1141
TYPE: DNA
ORGANISM: Homo sapiens
US-10-205-823-412

Query Match 60.7%; Score 802.2; DB 15; Length 1141;
Best Local Similarity 98.4%; Pred. No. 1.3e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

499 TTTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558
77 TCTCCTCGGAACACGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136
559 GGTGATGATGGTGTGTGTGATCAGTGCTGCTGAGCACTACAAAGTGTCTGC 618
137 GGTGATGATGGTGTGTGTGATCAGTGCTGCTGAGCACTACAAAGTGTCTGC 196
619 ACGTCTTTCATCAGCGGCACAGCCAGCGGCGGAGAGAGATGCTGCTCCTCAGA 678
197 ACGTCTTTCATCAGCGGCACAGCCAGCGGCGGAGAGAGATGCTGCTCCTCAGA 256
679 AGGATGCTGTGGCCCTCGGAGAGCAGATGTGAGCAACGGAATCCAGAGCGCAGGT 738
257 AGGATGCTGTGGCCCTCGGAGAGCAGATGTGAGCAACGGAATCCAGAGCGCAGGT 316
739 CTAGCGCCCGCTCGGCGCCACAGACCGCTGGCGCTGCGCCCTTGGCCAGCGGAGCG 798
317 CTAGCGCCCGCTCGGCGCCACAGACCGCTGGCGCTGCGCCCTTGGCCAGCGGAGCG 376
799 CTTCACCGCTTCAGCGCCACCTATCGTACCTGCGAGCAGATCGACCTGCCACCCAC 858
377 CTTCACCGCTTCAGCGCCACCTATCGTACCTGCGAGCAGATCGACCTGCCACCCAC 436
859 CATCTCGCTCTCAGACGGGAGAGCCGCCACCTACCGAGGCGCCCTGACCCCTCCAGCT 918
437 CATCTCGCTCTCAGACGGGAGAGCCGCCACCTACCGAGGCGCCCTGACCCCTCCAGCT 496
919 TCGGAGACCCCGAGCAGCTGGAACCTGAACCGGAGTGGTGGCGCACCCCAACAG 978
497 TCGGAGACCCCGAGCAGCTGGAACCTGAACCGGAGTGGTGGCGCACCCCAACAG 556
979 AACATCTTCAGACGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
557 AACATCTTCAGACGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
1039 CAGTAACTTCGGGGATCAGCGCCACGTCTACGCGGCGGCGGCGATGAGAGGGCGGCC 1098
617 CAGTAACTTCGGGGATCAGCGCCACGTCTACGCGGCGGCGGCGATGAGAGGGCGGCC 676
1099 GCCACCTACAGGAGGTCTATCGGCCACTACCGGGGCTCTCTTCAGACACAGCAGAG 1158
677 GCCACCTACAGGAGGTCTATCGGCCACTACCGGGGCTCTCTTCAGACACAGCAGAG 736
1159 CAGTGGCGCGCTCTCTTGTGAGGGGAACCGGCTCCACACACACATCGCGGCCCT 1218

737 CAGTGGCGCGCTCTCTTGTGAGGGGAGCCGGCTCCACCACACACATCGCGCCCT 796
1219 AGAGAGCGCAGCCATCTCGAGCAAAAGAGAGGATAAACAGAAAGGACACCTCTCTAGGG 1278
797 AGAGAGCGCAGCCATCTCGAGCAAAAGAGAGGATAAACAGAAAGGACACCTCTCTAGGG 856
1279 TCCCCAGGGGGCGCGGCTGGGCTGGCTAGGTGAAAGGCGAG 1321
857 TCCCCAGGGGGCGCGGCTGGGCTGGCTAGGTGAAAGGCGAG 899

RESULT 11
US-10-301-822-208
Sequence 208, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208
LENGTH: 1141
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (96)...(854)
US-10-301-822-208

Query Match 60.7%; Score 802.2; DB 15; Length 1141;
Best Local Similarity 98.4%; Pred. No. 1.3e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

499 TTTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558
77 TCTCCTCGGAACACGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136
559 GGTGATGATGGTGTGTGTGATCAGTGCTGCTGAGCACTACAAAGTGTCTGC 618
137 GGTGATGATGGTGTGTGTGATCAGTGCTGCTGAGCACTACAAAGTGTCTGC 196
619 ACGTCTTTCATCAGCGGCACAGCCAGCGGCGGAGAGAGATGCTGCTCCTCAGA 678
197 ACGTCTTTCATCAGCGGCACAGCCAGCGGCGGAGAGAGATGCTGCTCCTCAGA 256
679 AGGATGCTGTGGCCCTCGGAGAGCAGATGTGAGCAACGGAATCCAGAGCGCAGGT 738
257 AGGATGCTGTGGCCCTCGGAGAGCAGATGTGAGCAACGGAATCCAGAGCGCAGGT 316
739 CTAGCGCCCGCTCGGCGCCACAGACCGCTGGCGCTGCGCCCTTGGCCAGCGGAGCG 798
317 CTAGCGCCCGCTCGGCGCCACAGACCGCTGGCGCTGCGCCCTTGGCCAGCGGAGCG 376
799 CTTCACCGCTTCAGCGCCACCTATCGTACCTGCGAGCAGATCGACCTGCCACCCAC 858

Db	377	CTTCCACCGCTTCGAGGCCCACTTATCCGTACTCTGGACGACGAGATCGACCTTGCCACCCAC	436
Qy	859	CATCTCGCTGTTCAGACGCGGGAGAGCCCCACCCCTACGAGGGCCCCCTGCACCCCTCCAGCT	918
Db	437	CATCTCGCTGTTCAGACGCGGGAGAGCCCCACCCCTACGAGGGCCCCCTGCACCCCTCCAGCT	496
Qy	919	TCGGGACCCCGAGCAGCAGCTGGAACTGMAACGGGAGTCCGTTCGCGCGCACCCCCAAAACAG	978
Db	497	TCGGGACCCCGAGCAGCAGCTGGAACTGMAACGGGAGTCCGTTCGCGCGCACCCCCAAAACAG	556
Qy	979	AACCATCTTCGACAGTCACTGATAGTCCAGGCTGGCGGGCCCCCTGCCGCCCCCGAG	1038
Db	557	AACCATCTTCGACAGTCACTGATAGTCCAGGCTGGCGGGCCCCCTGCCGCCCCCGAG	616
Qy	1039	CAGTAACTCGGGGCATCAGCGCCACGTCGTACGGCAGCGCGGGCGGCATGAGAGGGGCCGCC	1098
Db	617	CAGTAACTCGGGGCATCAGCGCCACGTCGTACGGCAGCGCGGGCGGCATGAGAGGGGCCGCC	676
Qy	1099	GCCCACTTACAGCGAGGTCACTCGGCCACTACCGGGGTCTCTCTTCAGACACACAGCAGAG	1158
Db	677	GCCCACTTACAGCGAGGTCACTCGGCCACTACCGGGGTCTCTCTTCAGACACACAGCAGAG	736
Qy	1159	CAGTGGGCCCGCCCTCTCTTGTTCGAGGGGACCCCGGCTCCACACACATCGCGGCCCT	1218
Db	737	CAGTGGGCCCGCCCTCTCTTGTTCGAGGGGACCCCGGCTCCACACACATCGCGGCCCT	796
Qy	1219	AGAGAGCGCAGCCATCTGGAGCAAGAAGAGATAAACAGAAAGGACACCCCTCTCTAGGG	1278
Db	797	AGAGAGCGCAGCCATCTGGAGCAAGAAGAGATAAACAGAAAGGACACCCCTCTCTAGGG	856
Qy	1279	TCGCCAGGGGGCGGGCTGGGCTGCGTAGGTGAAAGGACAG	1321
Db	857	TCGCCAGGGGGCGGGCTGGGCTGCGTAGGTGAAAGGACAG	899

RESULT 12

```

US-10-241-220-44
; Sequence 44, Application US/10241220
; Publication NO. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-44

```

Db	197	ACGCTCCTTCATCAGCCGGCACA	CGCCAGGCGCGAGGAGAAATGCCTGTCTCAGA	256	
Qy	679	AGGATGCTGTGGCCCTCGGAGAGCA	CAGTGTCTCAGGCAA	CGGAATCCGACAGCCGCAAGT	738
Db	257	AGGATGCTGTGGCCCTCGGAGAGCA	CAGTGTCTCAGGCAA	CGGAATCCGAGHGCCGCAAGT	316
Qy	739	CTACGCCCCCGCTTCGGCCCA	CCGACCGCCTTGGCCGTGCGGCCCTTCGCCCCACGCGGGAGCG	798	
Db	317	CTACGCCCCCGCTTCGGCCCA	CCGACCGCCTTGGCCGTGCGGCCCTTCGCCACGCGGGAGCG	376	
Qy	799	CTTCCACGGCTTCAGCGCCCA	CCCTATCCGTACTCTGCAGGACGAGATCGACCTGCCACCCAC	858	
Db	377	CTTCCACGGCTTCAGCGCCCA	CCCTATCCGTACTCTGCAGGACGAGATCGACCTGCCACCCAC	436	
Qy	859	CATCTCGCTGTCAACGGGAGGAG	CCCCCACCCCTACGAGGGCCCTTGACCCCTCCAGCT	918	
Db	437	CATCTCGCTGTCAACGGGAGGAG	CCCCCACCCCTACGAGGGCCCTTGACCCCTCCAGCT	496	
Qy	919	TCGGGACCCCGAGCAGCAGCT	TGGAACTGAA	CCGGAGTCGGTGC	978
Db	497	TCGGGACCCCGAGCAGCAGCT	TGGAACTGAA	CCGGAGTCGGTGC	556
Qy	979	AACCATCTTCGACAGTCA	CACTGATGGATAGTGC	CAGSCTGGCGGCCCTTCGCCCCCCAG	1038
Db	557	AACCATCTTCGACAGTCA	CACTGATGGATAGTGC	CAGSCTGGCGGCCCTTCGCCCCCCAG	616
Qy	1039	CAGTAACTTCGGGATCAGCG	CCACGTCTACTCGGCAGCGCGGGCGCATGAGGGGGCGCC	1098	
Db	617	CAGTAACTTCGGGATCAGCG	CCACGTCTACTCGGCAGCGCGGGCGCATGAGGGGGCGCC	676	
Qy	1099	GCCCACTTACAGCGAGGTCA	TCGGCCACTACCGGGGTCTCTCTTCAGACACGACGAG	1158	
Db	677	GCCCACTTACAGCGAGGTCA	TCGGCCACTACCGGGGTCTCTCTTCAGACACGACGAG	736	
Qy	1159	CAGTGGGCCCGCCCTCCTT	GTGTGAGGGGACCGCGCTCCACACACACATCGGGCCCT	1218	
Db	737	CAGTGGGCCCGCCCTCCTT	GTGTGAGGGGACCGCGCTCCACACACACATCGGGCCCT	796	
Qy	1219	AGAGAGCGCAGCCATCT	TGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTCTAGGG	1278	
Db	797	AGAGAGCGCAGCCATCT	TGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTCTAGGG	856	
Qy	1279	TCGCCAGGGGGCGGGCTGGG	CTGCGTAGGTGAAAGGCAG	1321	
Db	857	TCGCCAGGGGGCGGGCTGGG	CTGCGTAGGTGAAAGGCAG	899	

RESULT 13

US-10-872-972-44
; Sequence 44, Application US/10872972
; Publication No. US2004022977A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872,972
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-872-972-44

```
Query Match      60.7%; Score 802.2; DB 18; Length 1850;
Best Local Similarity 98.4%; Pred. No. 1.3e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 499 TTTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558
Db 77 TCTCTCGGAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136
Qy 559 GGTGATGATGGTGTGATGATCAGTGCCTGTGAGCCACTACAAGCTGTCTGC 618
Db 137 GGTGATGATGGTGTGATGATCAGTGCCTGTGAGCCACTACAAGCTGTCTGC 196
Qy 619 ACAGTCTTTCATCAGCGGCACAGCCAGGGGCGAGAGAGATGCCCTGTCTCAGA 678
Db 197 ACAGTCTTTCATCAGCGGCACAGCCAGGGGCGAGAGAGATGCCCTGTCTCAGA 256
Qy 679 AGGATGCTGTGGCCCTCGAGAGACAGTGTCAAGGCAACGGATCCAGAGCGCAGGT 738
Db 257 AGGATGCTGTGGCCCTCGAGAGACAGTGTCAAGGCAACGGATCCAGAGCGCAGGT 316
Qy 739 CTAGCCCGCGCTCGGCCACCGACCGCTGGCGGTGCGGCCCTTCGCCAGGGGAGCG 798
Db 317 CTAGCCCGCGCTCGGCCACCGACCGCTGGCGGTGCGGCCCTTCGCCAGGGGAGCG 376
Qy 799 CTTCCACCGCTTCAGGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 858
Db 377 CTTCCACCGCTTCAGGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 436
Qy 859 CATCTCGCTGTACAGCGGAGGAGCCCCACCTTACAGGGGCCCTGACCCCTCCAGCT 918
Db 437 CATCTCGCTGTACAGCGGAGGAGCCCCACCTTACAGGGGCCCTGACCCCTCCAGCT 496
Qy 919 TCGGGACCCCGAGCAGCTGGAACCTGAAACCGGGAGTCTGGTGGCGCACCCCCAAGAG 978
Db 497 TCGGGACCCCGAGCAGCTGGAACCTGAAACCGGGAGTCTGGTGGCGCACCCCCAAGAG 556
Qy 979 AACCATCTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
Db 557 AACCATCTTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
Qy 1039 CAGTAACTCGGGCATCAGCGCCACCTGCTACCGGAGTGGTGGCGCACCCCCAAGAG 1098
Db 617 CAGTAACTCGGGCATCAGCGCCACCTGCTACCGGAGTGGTGGCGCACCCCCAAGAG 676
Qy 1099 GCCACCTTACAGCGAGTGTATCGGCCACTACCGGGGTCTCTTCCAGCACCAGCAGAG 1158
Db 677 GCCACCTTACAGCGAGTGTATCGGCCACTACCGGGGTCTCTTCCAGCACCAGCAGAG 736
Qy 1159 CAGTGGGCGCGCTCTTGTGAGGGGACCCGGCTCCACACACACACATCGCGCCCT 1218
Db 737 CAGTGGGCGCGCTCTTGTGAGGGGACCCGGCTCCACACACACACATCGCGCCCT 796
Qy 1219 AGAGAGCGCGCATCTGAGGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTTAGGG 1278
Db 797 AGAGAGCGCGCATCTGAGGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTTAGGG 856
Qy 1279 TCCCCAGGGGGCGGGCTGGGGCTGGTGAAGAGCAG 1321
Db 857 TCCCCAGGGGGCGGGCTGGGGCTGGTGAAGAGCAG 899
```

RESULT 14

US-10-872-991-44

```
; Sequence 44, Application US/10872991
; Publication No. US20040242860A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
```

```
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872,991
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-991-44
```

```
Query Match      60.7%; Score 802.2; DB 18; Length 1850;
Best Local Similarity 98.4%; Pred. No. 1.3e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
Qy 499 TTTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558
Db 77 TCTCTCGGAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136
Qy 559 GGTGATGATGGTGTGATGATCAGTGCCTGTGAGCCACTACAAGCTGTCTGC 618
Db 137 GGTGATGATGGTGTGATGATCAGTGCCTGTGAGCCACTACAAGCTGTCTGC 196
Qy 619 ACAGTCTTTCATCAGCGGCACAGCCAGGGGCGAGAGAGATGCCCTGTCTCAGA 678
Db 197 ACAGTCTTTCATCAGCGGCACAGCCAGGGGCGAGAGAGATGCCCTGTCTCAGA 256
Qy 679 AGGATGCTGTGGCCCTCGAGAGACAGTGTCAAGGCAACGGATCCAGAGCGCAGGT 738
Db 257 AGGATGCTGTGGCCCTCGAGAGACAGTGTCAAGGCAACGGATCCAGAGCGCAGGT 316
Qy 739 CTAAGCCCGCGCTTCGGGCCACCGACCGCTGGCGGTGCGGCCCTTCGCCAGGGGAGCG 798
Db 317 CTAAGCCCGCGCTTCGGGCCACCGACCGCTGGCGGTGCGGCCCTTCGCCAGGGGAGCG 376
Qy 799 CTTTCCACCGCTTCAGCGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 858
Db 377 CTTTCCACCGCTTCAGCGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 436
Qy 859 CATCTCGCTGTACAGCGGAGGAGCCCCACCTTACAGGGGCCCTGACCCCTCCAGCT 918
Db 437 CATCTCGCTGTACAGCGGAGGAGCCCCACCTTACAGGGGCCCTGACCCCTCCAGCT 496
Qy 919 TCGGGACCCCGAGCAGCTGGAACCTGAAACCGGGAGTGGTGGCGCACCCCCAAGAG 978
Db 497 TCGGGACCCCGAGCAGCTGGAACCTGAAACCGGGAGTGGTGGCGCACCCCCAAGAG 556
Qy 979 AACCATCTTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
Db 557 AACCATCTTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
Qy 1039 CAGTAACTCGGGCATCAGCGCCACCTGCTACCGGAGTGGTGGCGCACCCCCAAGAG 1098
Db 617 CAGTAACTCGGGCATCAGCGCCACCTGCTACCGGAGTGGTGGCGCACCCCCAAGAG 676
Qy 1099 GCCACCTTACAGCGAGTGTATCGGCCACTACCGGGGTCTCTTCCAGCACCAGCAGAG 1158
Db 677 GCCACCTTACAGCGAGTGTATCGGCCACTACCGGGGTCTCTTCCAGCACCAGCAGAG 736
Qy 1159 CAGTGGGCGCGCTCTTGTGAGGGGACCCGGCTCCACACACACACATCGCGCCCT 1218
Db 737 CAGTGGGCGCGCTCTTGTGAGGGGACCCGGCTCCACACACACACATCGCGCCCT 796
Qy 1219 AGAGAGCGCGCATCTGAGGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTTAGGG 1278
Db 797 AGAGAGCGCGCATCTGAGGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTTAGGG 1278
Qy 1279 TCCCCAGGGGGCGGGCTGGGGCTGGTGAAGAGCAG 1321
Db 857 TCCCCAGGGGGCGGGCTGGGGCTGGTGAAGAGCAG 856
```


Qy 1279 TCCCAGGGGGCCGGCTGGGCTGCCGTAGGTGAAGGCAG 1321
|||||
Db 857 TCCCAGGGGGCCGGCTGGGCTGCCGTAGGTGAAGGCAG 899
|||||

RESULT 15

```

US-09-821-812-2
; Sequence 2, Application US/09821812
; Publication NO. US20030166520A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Biaoyang
; TITLE OF INVENTION: Androgen Regulated Prostate Specific
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE: P-IS 4373
; CURRENT APPLICATION NUMBER: US/09/821,812
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)..(851)
US-09-821-812-2

```

Query Match 60.7%; Score 802.2; DB 10; Length 4527;
Best Local Similarity 98.4%; Pred. No. 1.3e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

499	QY	TTTTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCTGCGGT	558
77	Db	TCTCCTCGCAAAACAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCTGCGGT	136
559	QY	GGTGATGATGGTATGGTGTGGTGATCACGTGCTCTGAGCCACTACAGAGCTGTCTGC	618
137	Db	GGTGATGATGGTATGGTGTGGTGATCACGTGCTCTGAGCCACTACAGAGCTGTCTGC	196
619	QY	ACGGTCTTTCATCAGCCGGCAGACCCAGGGGGCGGAGGAGAGATGCCCTGTCTCAG	678
197	Db	ACGGTCTTTCATCAGCCGGCAGACCCAGGGGGCGGAGGAGAGATGCCCTGTCTCAG	255
679	QY	AGGATCGCTGTGCGCCCTCGSAGAGCACAGTGTTCAGGCCACGGGAATCCAGAGCGCGAGGT	738
257	Db	AGGATCGCTGTGCGCCCTCGSAGAGCACAGTGTTCAGGCCACGGGAATCCAGAGCGCGAGGT	316
739	QY	CTACGCCCGCCCTCGGCCCAACCGACCGCTTGGCGCTTGGCCCTTGGCCAGCGGGAGCG	798
317	Db	CTACGCCCGCCCTCGGCCCAACCGACCGCTTGGCGCTTGGCCCTTGGCCAGCGGGAGCG	376
799	QY	CTTCCACCGCTTCCAGCCCACTTATCGTACCTGACGACGAGATCGACCTGCCACCCAC	858
377	Db	CTTCCACCGCTTCCAGCCCACTTATCGTACCTGACGACGAGATCGACCTGCCACCCAC	436
859	QY	CATCTCGCTGTACAGCGGGAGAGCCCCACCTTACCAGGGCCCTTGCACTTCCAGCT	918
437	Db	CATCTCGCTGTACAGCGGGAGAGCCCCACCTTACCAGGGCCCTTGCACTTCCAGCT	496
919	QY	TGGGACCCCGAGCAGCTGTGAACTGTAAACCGGAGTGGTGGCGGCACCCGCCAACAG	978
497	Db	TGGGACCCCGAGCAGCTGTGAACTGTAAACCGGAGTGGTGGCGGCACCCGCCAACAG	556
979	QY	AACCATCTTCGACAGTGAAGCTGTATGATAGTGCAGGCTGGGCGGCCCTTGGCCCCCAG	1038
557	Db	AACCATCTTCGACAGTGAAGCTGTATGATAGTGCAGGCTGGGCGGCCCTTGGCCCCCAG	616
1039	QY	CAGTAATCTGGGCATCAGCGGCCACGTGTACGACGGCGGCGCATGGAGGGGCGCC	1098
617	Db	CAGTAATCTGGGCATCAGCGGCCACGTGTACGACGGCGGCGCATGGAGGGGCGCC	676
1099	QY	GCCCACTTACGCGAGGTTCATGGGCCACTACCGGGGTCTCTTTCAGCACACAGCAG	1158

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 10:31:50 ; Search time 4154.31 Seconds
(without alignments)
12103.794 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcggagcga.....ctgcgtagtgaaagcag 1321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	859.4	65.1	1005	1	AL578575
C 2	858.8	65.0	1038	1	AL517150
C 3	766.8	58.0	967	5	BQ641849 AGENCOURT
C 4	766	58.0	1046	5	BM922276 AGENCOURT
C 5	764.2	57.9	1059	1	AL543170
C 6	741	56.7	901	3	CR612083
C 7	736.4	55.7	916	5	BQ954555
C 8	734.2	55.6	850	1	AL558881
C 9	715	54.1	867	5	BX362396
C 10	714.6	54.1	897	1	AL558882
C 11	691.2	52.3	945	5	BUS39219
C 12	686.6	52.0	850	5	BUS39219
C 13	651	49.3	780	9	AY419334
C 14	630.6	47.7	1207	3	AK008976
C 15	618.6	46.8	1079	3	BC023092
C 16	614.6	46.5	782	5	BQ015170
C 17	607.4	46.0	609	5	BQ636742
C 18	588.8	44.6	605	7	CQ028567
C 19	578.4	43.8	890	5	BQ690750
C 20	570.4	43.2	973	5	BU169156
C 21	568.8	43.1	572	5	BX641317
C 22	567.4	43.0	729	5	BQ575741
C 23	564.8	42.8	730	4	BM677602
C 24	563.2	42.6	728	5	BU683523

25	550	41.6	551	4	BM141979
26	529.8	40.1	894	4	BI851941
27	521	39.4	1068	5	BUS27705
28	507	38.4	780	9	AY419335
29	501.6	38.0	588	4	BM483503
30	493.6	37.4	693	1	AI761441
31	493.4	37.4	655	5	BQ691705
32	487.6	36.9	646	9	CG784226
33	486	36.8	1400	4	BM559329
34	480.8	36.4	964	5	BUS59860
35	477.6	36.2	646	5	BUS59841
36	476.4	36.1	651	6	CB554226
37	475.2	36.0	624	9	AY419336
38	468.8	35.5	1280	5	BQ691500
39	468	35.4	857	4	EG323347
40	468	35.4	974	2	BB624904
41	465.8	35.3	744	5	BU414421
42	461	34.9	763	4	BI646175
43	455.4	34.5	629	5	BU730650
44	452.2	34.2	618	6	CD367193
45	448	33.9	626	5	BM974296

ALIGNMENTS

RESULT 1
AL578575/c
LOCUS AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens EST 07-APR-2004
DEFINITION CDNA clone CS0DK001YC24 3-PRIME, mRNA sequence.
ACCESSION AL578575
VERSION AL578575.3 GI:46257448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1005)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31316780.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945_r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?S=CS0DK001BB12NP1&c=9945.r.

FEATURES

source
1..1005
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK001YC24"
/cell_type="HELA"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 65.1%; Score 859.4; DB 1; Length 1005;
Best Local Similarity 97.7%; Pred. No. 7.1e-150;
Matches 882; Conservative 9; Mismatches 10; Indels 2; Gaps 2;


```

Db      481  |||||||ACGTCCTACGGCAGCGGGGGCGCATGGAGGGGGCGCGCCACCTACAGCGAGTCAATC 540
Qy      1121  |||||||GCCCACTACCGGGGCTCTCTTCCAGCACAGCAGACAGTGGGGCGCCCTCTTCTGCTG 1180
Db      541  |||||||GCCCACTACCGGGGCTCTCTTCCAGCACAGCAGACAGTGGGGCGCCCTCTTCTGCTG 600
Qy      1181  |||||||GAGGGAGCCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGC 1240
Db      601  |||||||GAGGGAGCCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGC 660
Qy      1241  |||||||AAAGAGAGGATTAACAGAAAGGACACCTCTTAGGGTCCCGAGGGGGCGGGCTGGG 1300
Db      661  |||||||AAAGAGAGGATTAACAGAAAGGACACCTCTTAGGGTCCCGAGGGGGCGGGCTGGG 720
Qy      1301  |||||||GCTCGTAGGTGAAAAGGCAG 1321
Db      721  |||||||GCTCGTAGGTGAAGAGGCAG 741

```

```

RESULT 7
BQ954555
LOCUS      916 bp mRNA linear EST 21-AUG-2002
DEFINITION AGNCOURT 8825282 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204609 5', mRNA sequence.
ACCESSION BQ954555
VERSION BQ954555.1 GI:22370033
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 916)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@femail.nih.gov

```

```

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

```

```

Plate: LLAM13626 row: c column: 10
High quality sequence stop: 669.

```

FEATURES

```

source
1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204609"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic_nerve"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
Not1; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGTCCG-3' and
5'-GACTAGTTCTAGATCCGAGCGCCCTCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

```

ORIGIN

```

Query Match 55.7%; Score 736.4; DB 5; Length 916;
Best Local Similarity 95.7%; Pred. No. 5.5e-127;
Matches 800; Conservative 0; Mismatches 31; Indels 5; Gaps 4;

```

```

Qy      344  |||||||GCCCGGCGGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 403
Db      1      |||||||GCCCGGCGGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 60
Qy      404  |||||||GCCCGGCTCATGACACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCG 463
Db      61  |||||||GCCCGGCTCATGACACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCG 120
Qy      464  |||||||CCCAATGTCTCTGCACTGTCGCAACTGCAAAAGCTCTTTGTTCCAGAGCATGGAGATCACG 523
Db      121  |||||||CCCAATGTCTCTGCACTGTCGCAACTGCAAAAGCTCTTTGTTCCAGAGCATGGAGATCACG 180
Qy      524  |||||||GACCTGAGTGTGTTCCAGATCATCATGCTGGTGGTGTGATGATGATGATGATGATGATG 583
Db      181  |||||||GAGCTGGAGTTTGTTCAGATCATCATGCTGGTGGTGTGATGATGATGATGATGATGATG 240
Qy      584  |||||||ATCACGTGCTGCTGAGCCACTACAGCTGTCTGACCGGTCTTTCATCAGCGGACAGC 643
Db      241  |||||||ATCACGTGCTGCTGAGCCACTACAGCTGTCTGACCGGTCTTTCATCAGCGGACAGC 300
Qy      644  |||||||CAGGGCGGAGAGAGAGATGCTCTCTCAGAGAGATGCTGTGGCCCTCGGAGAGC 703
Db      301  |||||||CAGGGCGGAGAGAGAGATGCTCTCTCAGAGAGATGCTGTGGCCCTCGGAGAGC 360
Qy      704  |||||||ACAGTGTCAAGGCAACGGAATCCAGAGCGCAGGTCTACGCCCGCGCTCGGCCACCGAC 763
Db      361  |||||||ACAGTGTCAAGGCAACGGAATCCAGAGCGCAGGTCTACGCCCGCGCTCGGCCACCGAC 420
Qy      764  |||||||CGCTGGCGCTGCCCGCTTCCGCCAGGGGAGCGCTTCCACCGCTTCCAGCGCCACCTAT 823
Db      421  |||||||CGCTGGCGCTGCCCGCTTCCGCCAGGGGAGCGCTTCCACCGCTTCCAGCGCCACCTAT 480
Qy      824  |||||||CGGTACCTGCAGCAGAGATGCACTGCCACCCACCATCTCGCTGTACAGCGGAGAG 883
Db      481  |||||||CGGTACCTGCAGCAGAGATGCACTGCCACCCACCATCTCGCTGTACAGCGGAGAG 540
Qy      884  |||||||CCCCCACCCTACAGGGGCGCCCTGCACCTTCCGAGCTTCCGGAGCCCCCGAGCAGCGTGGAA 943
Db      541  |||||||CCCCCACCCTACAGGGGCGCCCTGCACCTTCCGAGCTTCCGGAGCCCCCGAGCAGCGTGGAA 600
Qy      944  |||||||CTGAACCGGGAGTGGTGGCGGCGACCCCAAGAGAACATCTTCGACAGTGAATGATG 1003
Db      601  |||||||CTGAACCGGGAGTGGTGGCGGCGACCCCAAGAGAACATCTTCGACAGTGAATGATG 660
Qy      1004  |||||||GATAGTGC-AGGCTGGGCGCGCCCTGCGCCCGGAGAGTAACTCGGCGATCAG-CGCCA 1061
Db      661  |||||||GATAGTGC-AGGCTGGGCGCGCCCTGCGCCCGGAGAGTAACTCGGCGATCAG-CGCCA 720
Qy      1062  |||||||CGTGTACGCGCAGCGCGGGC-GCATGGAGGGCGCGCGCCACCTACAGCGAGGTCAATC 1120
Db      721  |||||||CGTGTACGCGCAGCGCGGGCGGCATGGAGGGGGCGCGCGCCCTTACACCGAGGTCAAT 780
Qy      1121  |||||||GGCCA--CTACCGGGGTCTCTCTTCAGACACAGCAGAGAGAGTGGGGCGCGCTCC 1174
Db      781  |||||||CGGCAACTAACCGGGGGCGCTGCTTTTACCGCGCGGAGAGAAACAGAGAGAGAGAGAG 836

```

```

RESULT 8
AL558881/c
LOCUS      850 bp mRNA linear EST 02-APR-2004
DEFINITION AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ015YF12 3-PRIME, mRNA sequence.
ACCESSION AL558881
VERSION AL558881.3 GI:46184268
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 850)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

```


JOURNAL
COMMENT

Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31283014.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DJ015DC06NP1&c=9945.r.

FEATURES

source

1. .850
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ015F12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 55.6%; Score 734.2; DB 1; Length 850;
Best Local Similarity 99.3%; Pred. No. 1.4e-126;
Matches 736; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 581 GTGATCAGCTGCTGTGAGCCACTCAAGCTGTGACGGTCTTTCATCAGCCGCGAC 640
DB 850 GTGATCAGCTGCTGTGAGCCACTCAAGCTGTGACGGTCTTTCATCAGCCGCGAC 791

QY 641 AGCCAGGGCGGAGGAGAGATGCCCTCTCTCAGAGGATGCTGTGGCCCTCGGAG 700
DB 790 AGCCAGGGCGGAGGAGAGATGCCCTCTCTCAGAGGATGCTGTGGCCCTCGGAG 731

QY 701 AGCAGAGTGTACGACACGGAATCCAGAGCCGAGGTACGCCCGGCTCGGCCACC 760
DB 730 AGCAGAGTGTACGACACGGAATCCAGAGCCGAGGTACGCCCGGCTCGGCCACC 671

QY 761 GACCGCTGCGCTGCGCCCTTCGCCAGCGGAGCGCTTCACCGCTTCAGAGCCACC 820
DB 670 GACCGCTGCGCTGCGCCCTTCGCCAGCGGAGCGCTTCACCGCTTCAGAGCCACC 611

QY 821 TATCCGTACCTGCAGACGAGATCGACCTGCCACCCACCATCTCGTGTGACAGCGGGAG 880
DB 610 TATCCGTACCTGCAGACGAGATCGACCTGCCACCCACCATCTCGTGTGACAGCGGGAG 551

QY 881 GAGCCGCCACCTTACAGGGCCCTGTGACCTCAGCTTCGGGACCCCGAGCAGAGCTG 940
DB 550 GAGCCGCCACCTTACAGGGCCCTGTGACCTCAGCTTCGGGACCCCGAGCAGAGCTG 491

QY 941 GAACCTGACCGGAGTGGTGGCGGACCCGCCAAACAGACCATCTTCGACAGTGACCTG 1000
DB 490 GAACCTGACCGGAGTGGTGGCGGACCCGCCAAACAGACCATCTTCGACAGTGACCTG 431

QY 1001 ATGGATAGTCCAGGCTGGCGGCCCTTCGCCCCCGACAGAGTAACCTCGGGCATCAGCGCC 1060
DB 430 ATGGATAGTCCAGGCTGGCGGCCCTTCGCCCCCGACAGAGTAACCTCGGGCATCAGCGCC 371

QY 1061 ACTGTGTACGGCAGCGCGCGGATGAGAGGGCGCGCCGCCACCTTACAGCGAGGTATC 1120
DB 370 ACTGTGTACGGCAGCGCGCGGATGAGAGGGCGCGCGCCGCCACCTTACAGCGAGGTATC 311

QY 1121 GGCCTACTACCGGGGCTCTCTTCCAGCACCAGCAGAGTGGCGGCCCTCTTGGCTG 1180
DB 310 GGCCTACTACCGGGGCTCTCTTCCAGCACCAGCAGAGTGGCGGCCCTCTTGGCTG 251

QY 1181 GAGGGACCCGGCTCCACCACACACACATCGCGCCCTAGAGAGCGGACCATCTGGAGC 1240
DB 250 GAGGGACCCGGCTCCACCACACACACATCGCGCCCTAGAGAGCGGACCATCTGGAGC 191

QY 1241 AAAGAGAAGGATAAACAAGAAAGACACCTCTCTAGGGTCCCCCAGGGGGCCGGGCTGGG 1300
DB 190 AAAGAGAAGGATAAACAAGAAAGACACCTCTCTAGGGTCCCCCAGGGGGCCGGGCTGGG 131

QY 1301 GCTGCGTAGGTGAAAAGGCAG 1321
DB 130 GCTGCGTAGGTGAAAAGGCAG 110

RESULT 9

BX362396/c

LOCUS

DEFINITION

Homo sapiens cDNA clone CS0DJ014YN15 3-PRIME, mRNA sequence.

ACCESSION

BX362396

VERSION

BX362396.2 GI:46307643

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 867)

AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

On May 5, 2003 this sequence version replaced gi:30378625.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

9945.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DJ014CG08NP1&c=9945.r.

Location/Qualifiers

1. .867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DJ014YN15"

/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"

/cell_line="JURKAT"

/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 54.1%; Score 715; DB 5; Length 867;

Best Local Similarity 96.2%; Pred. No. 5.3e-123;

Matches 731; Conservative 16; Mismatches 11; Indels 2; Gaps 2;

QY 563 ATGATGGTATGTGGTGGTGATC-ACGTGCGCTGTGAGCCACTACAGCTGTCTGCACG 621

DB 867 ATGATGGTATGTGGTGGTGATCTCGTGGCTGTGAGCCATTACAGCTGTCTGCACG 808

QY 622 GTCCTTTCATCAGCCGACACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGAAGG 681

DB 807 GTCCTTTCATCAGCCGACACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGAAGG 748

QY 682 ATGCTGTGGCCCTCGGAGGACAGTGTGACGCAACGGAATCCAGAGCCGCGAGTCTTA 741

DB 741


```
Db 747 ATGCTTGTGGCCYTCGGAGAGACAGTGTCTAGGCAACGGAATCCAGAGCCGCA-GTYTA 689
Qy 742 CGCCCGCTCGGCCACCGACCGCTCGCGCTGCGGCTTTCGCCACAGCGGAGCGCTT 801
Db 688 CGCCCGCTTGGGCCACCGACCGCTGCGGCTTTCGCCACAGCGGAGCGCTT 629
Qy 802 CCACCGCTTCAGGCCACCTATTCGTCTCTGACGACGAGATCGACCTGCCACCCACAT 861
Db 628 CCACCGCTTCAGGCCACCTATTCGTCTCTGACGACGAGATCGACCTGCCACCCAT 569
Qy 862 CTCGCTGTACAGCGGAGGAGCCGCCACCTACAGGCGCCCTGACCCCTCCAGCTTCG 921
Db 568 CTCGCTGTACAGCGGAGGAGCCGCCACCTACAGGCGCCCTGACCCATCMAGTTTCG 509
Qy 922 GGACCCCGAGCAGCAGCTGGAACCTGAACCGGAGTTCGTGCGCGCACCCCAACAGAAC 981
Db 508 GGACCCCGAGCAGCAGCTGGAACCTGAACCGGAGTTCGTGCGCGCACCCCAACAGAAC 449
Qy 982 CATCTTCAGCAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1041
Db 448 CATCTTCAGCAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 389
Qy 1042 TAACTTCGGGATCAGCGCAGCTGCTAGCGGAGTTCGTGCGCGCACCCCAACAGAAC 1101
Db 388 TAACTTCGGGATCAGCGCAGCTGCTAGCGGAGTTCGTGCGCGCACCCCAACAGAAC 329
Qy 1102 CACTACAGCAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1161
Db 328 CACTACAGCAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 269
Qy 1162 TGGGCGCGCTCTCTGCTGAGGGGACCGGCTCCACACACACACACACACACACAC 1221
Db 268 TGGGCGCGCTCTCTGCTGAGGGGACCGGCTCCACACACACACACACACACAC 209
Qy 1222 GAGCGCAGCCTATCGGAGCAAGAGAGAGATTAACAGAAAGGACACCTCTCTAGGTC 1281
Db 208 GAGCGCAGCCTATCGGAGCAAGAGAGAGATTAACAGAAAGGACACCTCTCTAGGTC 149
Qy 1282 CCAGGGGGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 1321
Db 148 CCAGGGGGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 109
```

RESULT 10

AL558882 897 bp mRNA linear EST 02-APR-2004
LOCUS AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DJ015YF12 5-PRIME, mRNA sequence.

AL558882
ACCESSION AL558882
VERSION 1
KEYWORDS EST.

AL558882.3 GI:46184269

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 897)

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31283015.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

9945.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DJ015DC06QP1&c=9945.r.

Location/Qualifiers

FEATURES

source

```
1. .897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ015YF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

```
Query Match 54.1%; Score 714.6; DB 1; Length 897;
Best Local Similarity 99.3%; Pred. No. 6.3e-123;
Matches 736; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

Qy 581 GTGATCAGTCGCTGCTGAGCCACTACAAGTCTCTGCAAGGTCCTTTCATCAGCCGCGAC 640
Db 1 GTGATCAGTCGCTGCTGAGCCACTACAAGTCTCTGCAAGGTCCTTTCATCAGCCGCGAC 60
Qy 641 AGCCAGGGCGGAGGAGAGAGATGCCCTGTCCTCAGAAAGGATGCTGTGGCCCTCGGAG 700
Db 61 AGCCAGGGCGGAGGAGAGAGATGCCCTGTCCTCAGAAAGGATGCTGTGGCCCTCGGAG 120
Qy 701 AGCACAGTGTTCAGGCAACCGAATCCAGAGCGCAGGTCTACGCCCGGCTCGGCCAC 760
Db 121 AGCACAGTGTTCAGGCAACCGAATCCAGAGCGCAGCA-GTCTACGCCCGGCTCGGCCAC 179
Qy 761 GACCGCTCGGCGCTGCGGCTTCGCCAGCGGAGCGCTTCACCGCTTCAGAGCCAC 820
Db 180 GACCGCTCGGCGCTGCGGCTTCGCCAGCGGAGCGCTTCACCGCTTCAGAGCCAC 239
Qy 821 TATCCGTACTTCAGCAGCAGATTCGACCTTCGCAACCCATCTTCGTGTTCAGAGGGAG 880
Db 240 TATCCGTACTTCAGCAGCAGATTCGACCTTCGCGGCCACCATCTTCGTGTTCAGAGGGAG 299
Qy 881 GAGCCCCACCTTACCAGGGCGCTTCGCCAGCTTCGAGTTTCGGGAGCCCGCAGGAGAGCTG 940
Db 300 GAGCCCCACCTTACCAGGGCGCTTCGCCAGCTTCGAGTTTCGGGAGCCCGCAGGAGAGCTG 359
Qy 941 GAACCTGAAACCGGAGTTCGCTGCGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTG 1000
Db 360 GAACCTGAAACCGGAGTTCGCTGCGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTG 419
Qy 1001 ATGGATAGTTCAGAGCTGGGCGGCGCTTCGCCAGCAGCAGTAACCTCGGGCATTCAGCGCC 1060
Db 420 ATGGATAGTTCAGAGCTGGGCGGCGCTTCGCCAGCAGCAGTAACCTCGGGCATTCAGCGCC 479
Qy 1061 AGCTGCTACGCGAGCGGCGGCGCATGGAGGGCGCGCCGCCACCTTACAGCGAGGTCATC 1120
Db 480 AGCTGCTACGCGAGCGGCGGCGCATGGAGGGCGCGCCGCCACCTTACAGCGAGGTCATC 539
Qy 1121 GGCCTACTACCGGGGTTCCTCTTCAGCAGCAGCAGCAGTGGGCGGCGCTTCCTTCCTGCTG 1180
Db 540 GGCCTACTACCGGGGTTCCTCTTCAGCAGCAGCAGCAGTGGGCGGCGCTTCCTTCCTGCTG 599
Qy 1181 GAGGGGACCGGCTCCACACACACATCGCGCGCTTCAGAGCGCAGCAGTCTTCGAGC 1240
Db 600 GAGGGGACCGGCTCCACACACACATCGCGCGCTTCAGAGCGCAGCAGTCTTCGAGC 658
Qy 1241 AAAGAGAGAGTAAACAGAAAGGACACCTCTCTTAGGGTCCCGAGGGGGCGGGCTGGG 1300
Db 659 AAAGAGAGAGTAAACAGAAAGGACACCTCTCTTAGGGTCCCGAGGGGGCGGGCTGGG 718
Qy 1301 GCTCGGTAGGTGAAAGGCAG 1321
Db 719 GCTCGGTAGGTGAAAGGCAG 739
```

RESULT 11

BUS39219
LOCUS
DEFINITION BUS39219 945 bp mRNA linear EST 13-SEP-2002
IMAGE:6569922 5', mRNA sequence.
ACCESSION BUS39219
VERSION BUS39219.1 GI:22849660
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 945)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2757 row: P column: 18
High quality sequence stop: 663.
Location/Qualifiers
1. .945
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6569922"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 107"
/note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

Query Match 52.3%; Score 691.2; DB 5; Length 945;
Best Local Similarity 93.7%; Pred.No. 1.4e-118;
Matches 764; Conservative 0; Mismatches 44; Indels 7; Gaps 4;
QY 499 TTGTGTTCCAGAGCATGCGAGCTGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558
DB 65 TCTCTCGGAACACGAGCAATGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 124
QY 559 GGTGATGATGTTGATGTTGTTGATCAGTGCCTGCTGAGCCTACAGCTGCTGC 618
DB 125 GGTGATGATGTTGATGTTGTTGATCAGTGCCTGCTGAGCCTACAGCTGCTGC 184
QY 619 ACGGTCTTCATCAGCGGCACAGCAGCGGCGGAGAGAGATGCTGCTCCTCAGA 678
DB 185 ACGGTCTTCATCAGCTGGCAGCAGCGGCGGAGAGAGATGCTGCTCCTCAGA 244
QY 679 AGGATGCTGTGCGCTTCGAGAGCAGTGTTCAGCAACGGAATCCAGAGCGCGAGT 738
DB 245 AGGATGCTGTGCGCTTCGAGAGCAGTGTTCAGCAACGGAATCCAGAGCGCGAGT 304
QY 739 CTACGCGCGCTTCGCGCCACACGCGCTGCGCGCTGCGCGCTTCGCGCGCGAGCG 798
DB 305 CTACGCGCGCTTCGCGCCACACGCGCTGCGCGCTGCGCGCTTCGCGCGCGAGCG 364
QY 799 CTTCACCGCTTCAGCGCCACCTATCGTACCTGACGACGAGATGCACTGCCACCCAC 858
DB 365 CTTCACCGCTTCAGCGCCACCTATCGTACCTGACGACGAGATGCACTGCCCGCCAC 424

QY 859 CATCTCGCTGTACAGCGGGAGAGCCCCACCTACAGGGCGCCCTGCACCTCCAGCT 918
DB 425 CATCTCGCTGTGAGCGGGAGAGAGCCCCACCTACAGGGCGCCCTGCACCTCCAGCT 484
QY 919 TCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTTCGGTGGCGCACCCCCCAACAG 978
DB 485 TCGGGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTTCGGTGGCGCACCCCCCAACAG 544
QY 979 AACCATCTTCGACAGTGAAGCTGATGATAGTGCAGGCTGGGCGGCCCTTCGCCCGCCAG 1038
DB 545 AACCATCTTCGACAGTGAAGCTGATGATAGTGCAGGCTGGGCGGCCCTTCGCCCGCCAG 604
QY 1039 CAGTAACTCGGGCATCAGCGCCACGCTGCTACGCGACGGGCGGCGCATGAGAGGGCGGCC 1098
DB 605 CAGTAACTCGGGCATCAGCGCCACGCTGCTACGCGACGGGCGGCGCATGAGAGGGCGGCC 664
QY 1099 GCCCAGCTACAGCGAGGTTCATCGGCCACTACCGGGGTCTCTCTCCAGCACCAGAGAG 1158
DB 665 GCCCAGCTACAGCGAGGTTCATCGGCCACTACCGGGGTCTCTCTCCAGCACCAGAGAG 724
QY 1159 CAGTGGCGCGCCCT-CTTTGCTGAGGGGACCGCGCTCCACCAACACATCGCG-CCC 1216
DB 725 CAGTGGCGCGCCCTCTCCCTTGTGGAGGGGACCGCGCTCCACCAACACATCGTGGCCC 784
QY 1217 CTAGAGAGCGCAG-CCATCTGGAGCAAGAGAGGATAA- ----CAGAAAGGACACCTC 1271
DB 785 CTAAGAGCGCAGCCCATCTGGAGCAAGAGAGGATAAACCCGAAAGGACACCTTC 844
QY 1272 TCTAGAGTCCCGAGGGGGCGCGGCTGGGCTGCG 1306
DB 845 TTCTAGTCCCCCGAGGGGGCGCGGCTGGG 879

RESULT 12
BUS39219
LOCUS
DEFINITION BUS39219 850 bp mRNA linear EST 20-SEP-2002
IMAGE:6497853 5', mRNA sequence.
ACCESSION BUS39219
VERSION BUS39219.1 GI:23254677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2679 row: i column: 22
High quality sequence stop: 499.
Location/Qualifiers
1. .850
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6497853"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 142"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggc);
Site 2: SfiI (ggcgcctcggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -

Db	446	AACTGAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCGACAGTGACCTGA	505
QY	1002	TGATAGTGCAGGCTGGGGGCGCCCTGCGCCCGCCAGCAAGTAACATCGGGCATCAGCGCCA	1061
Db	506	TGATAGTGCAGGCTGGGGGCGCCCTGCGCCCGCCAGCAAGTAACATCGGGCATCAGCGCCA	565
QY	1062	CGTGCTACGCGGCGGCGGCGCATGGAGGGGCGCGCCAGCAAGTAACATCGGGCATCAGCGCCA	1121
Db	566	CGTGCTACGCGGCGGCGGCGCATGGAGGGGCGCGCCAGCAAGTAACATCGGGCATCAGCGCCA	625
QY	1122	GCCACTACCGGCGGCTCTCTCCAGCACACAGCAGCAGTGGGCGCGCCCTCTCTGCTGG	1181
Db	626	GCCACTACCGGCGGCTCTCTCCAGCACACAGCAGCAGTGGGCGCGCCCTCTCTGCTGG	685
QY	1182	AGGGGACCGGCTCTCCACACACACATCGCGCCCTTAGAGCGCGCATCTCGAGCA	1241
Db	686	AGGGGACCGGCTCTCCACACACACATCGCGCCCTTAGAGCGCGCATCTCGAGCA	745
QY	1242	AACAGAGGATTAACAGAGGACACCTCTCTAG	1276
Db	746	AACAGAGGATTAACAGAGGACACCTCTCTAG	780
RESULT 14			
AK008976			
LOCUS			
DEFINITION	AK008976	1207 bp mRNA linear	HTC 03-APR-2004
ACCESSION	AK008976		
VERSION	AK008976.1	GI:12843488	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	Carninci, P. and Hayashizaki, Y.		
MEDLINE	High-efficiency full-length cDNA cloning		
PUBMED	Meth. Enzymol. 303, 19-44 (1999)		
AUTHORS	99279253		
TITLE	10349636		
JOURNAL	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
MEDLINE	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
PUBMED	Normalization and subtraction of cap-trapper-selected cDNAs to		
AUTHORS	prepare full-length cDNA libraries for rapid discovery of new genes		
TITLE	Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL	20499374		
MEDLINE	11042159		
PUBMED	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
AUTHORS	Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,		
TITLE	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		
JOURNAL	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		
MEDLINE	Fujikake, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watahiki, M.,		
PUBMED	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
AUTHORS	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format		
JOURNAL	sequencing pipeline with 384 multicapillary sequencer		
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	20530913		
AUTHORS	11076861		
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the		
JOURNAL	PANTOM Consortium.		
MEDLINE	Functional annotation of a full-length mouse cDNA collection		
PUBMED	Nature 409, 685-690 (2001)		
AUTHORS	5		
TITLE	The PANTOM Consortium and the RIKEN Genome Exploration Research		
JOURNAL	Group Phase I & II Team.		
MEDLINE	Analysis of the mouse transcriptome based on functional annotation		
PUBMED	of 60,770 full-length cDNAs		

JOURNAL REFERENCE AUTHORS	Nature 420, 563-573 (2002)			
	6 (bases 1 to 1207)			
TITLE JOURNAL	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.			
	Direct Submission			
COMMENT	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, Japan (E-mail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)			
	Please visit our web site (http://genome.gsc.riken.jp/) for further details.			
FEATURES source	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATTAATTAATCCCGCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.			
	Host: SOLR.			
FEATURES CDs	Location/Qualifiers			
	1. .1207 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM DB:2210418102" /db_xref="taxon:10090" /clone="2210418102" /sex="male" /tissue type="stomach" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 391. .1173 /note="unnamed protein product; Nedda 4W binding protein 4 (MGDI:1929600) putative" /codon_start=1 /protein_id="BAB26001.1" /db_xref="GI:12843489" /translation="MSPARATQRLSPFSEITELEFQIVIVVVMVMMVMTCLL SHYLSARSFIRHSQARRDGLSEGLWPSESTVSGMPEPQYAPAPDRDLRLAV PFPIQRSFPQYVLOHEIALPPTISLSDGPPPPYQGPCTQLQADPQQLNELNES VRAPNRITFDSLDISTWLGCPSPNSGTSATCYSSGGRMEGPPPYSEVIGHYP GSSFQHQSGNGPSSLLGTRLHSHIAPLENKEKQKHPL"			
ORIGIN	Query Match 47.7%; Score 630.6; DB 3; Length 1207;			
	Best Local Similarity 82.4%; Pred. No. 2.7e-107;			
Qy	Matches 782; Conservative 0; Mismatches 139; Indels 28; Gaps 4;			
	346 GC CGCGCGGAGCCCCCG			

QY 466 CAATGTCCTCTGACGTGCACTG-CAAACGGCTCTTTGTTCCAGAGCATGGAGATCACGG 524
 Db 389 CAATGTCCTCTGGGTGCACTGCGCCAGCGCTCTTTGTTCCAGAGCATGGAGATCACGG 448
 QY 525 AGCTGGAGTTGTTGAGATCATCATCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 584
 Db 449 AGCTGGAGTTGTTGCAAACTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 508
 QY 585 TCACGTGCTGCTGAGCAGCACTACAGCTGCTGACGGTCTCTTCAATCAGCGGACAGCC 644
 Db 509 TTAGTGGCTGCTGAGCAGCACTACAGCTGCTGAGCGGCTCTTCAATCAGCGGACAGCC 568
 QY 645 AGGGCGGAGGAGAGAGATGCCCTGCTCTCAGAAAGATGCTGCTGGCCCTCGGAGAGCA 704
 Db 569 AGGCGAGGAGGAGAGAGATGCCCTGCTCGAAGATGCTCTGGCCCTCAGAGAGTA 628
 QY 705 CAGTCTCAGGCAACCGAATCCAGAGCGGAGTCTACGCCCGGCTCGGCCCAACCGAC 764
 Db 629 CGGTGTGAGG---TGAATGCGGAGGACAGGTCTATGCCCGGCTCGGCCCACTGACC 685
 QY 765 GCTCGGCGGTGCGGCGCTTTCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTATC 824
 Db 686 GACTCGCTGCTGCGGCGCTTTCAGCGG-----AGCGAATCCAAACCCACCTAC 736
 QY 825 GGTACTCGAGCAGAGATGCACTGCGCCACCCCAATCTGCTCTCAGAGCGGAGGAGC 884
 Db 737 CTTACTCGAGCAGAAATGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 796
 QY 885 CCCACCTTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 944
 Db 797 CCCACCTTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 856
 QY 945 TGAACCGGAGTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1004
 Db 857 TGAACCGGAGTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 916
 QY 1005 ATAGTGCAGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1064
 Db 917 ACAGACCATGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 976
 QY 1065 GCTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1124
 Db 977 GCTACGAGCGGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1036
 QY 1125 ACTACCGGCGGCTCTCTTCCAGCAGCAGAGAGTGGGCGGCGGCGGCGGCGGCGGCGG 1184
 Db 1037 ACTACCGGCGGCTCTCTTCCAGCAGCAGAGAGTGGGCGGCGGCGGCGGCGGCGGCGG 1096
 QY 1185 GGACCGGCGTCCACACACACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1244
 Db 1097 GGACCGGCGTCCATCTCGACATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1141
 QY 1245 AGAAGGATAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGCGGCGGCGGCGGCGG 1293
 Db 1142 AGAAGGATAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGCGGCGGCGGCGGCGG 1190

RESULT 15
 BC023092
 LOCUS
 DEFINITION BC023092 1079 bp mRNA linear HTC 20-SEP-2002
 Mus musculus, Nedd4 WW binding protein 4, clone IMAGE:398996,
 mRNA.
 ACCESSION BC023092
 VERSION BC023092.1 GI:18605637
 KEYWORDS HTC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1079)
 AUTHORS Strausberg,R.
 TITLE Direct Submission

JOURNAL

REMARK
COMMENT

Submitted (04-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 36 Row: h Column: 6
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
 This clone has the following problem: frame shifted.

FEATURES
source

1..1079
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:398996"
 /tissue_type="Mammary tumor metastasized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMV."
 /clone_lib="NCI CGAP_Lu29"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 46.8%; Score 618.6; DB 3; Length 1079;
 Best Local Similarity 84.5%; Pred. No. 4,6e-105;
 Matches 741; Conservative 0; Mismatches 109; Indels 27; Gaps 3;
 QY 417 ACCGCTTGTGATGGGGTCAACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 476
 Db 15 ACCGCTTGTGATGGGGTCAACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 74
 QY 477 GCACGTGCAACTGCAGAAAGCTCTTTGTTCCAGAGCATGGAGATCACGAGCTGGAGTTTG 536
 Db 75 GCGCGTCAACTGCAGCGCTCTTTGTTCCAGATGGAGATCACGAGCTGGAGTTTG 134
 QY 537 TTCAGATCATCATCATGCTGT 596
 Db 135 TCCAAATCGT 194
 QY 597 TGAGCCACTACAAGCTGTCTGACGGTCTTCATCAGCGGCGGCGGCGGCGGCGGCGGCGG 656
 Db 195 TGAGCCACTACAAGCTGTCTGACGGTCTTCATCAGCGGCGGCGGCGGCGGCGGCGGCGG 254
 QY 657 GAGAAGATGCCCTGTCTCTCAGAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 716
 Db 255 GAGACGATGAGTCTCTCTCGAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 312
 QY 717 ACAGAAATCCAGAGCGGCGGCTGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 776
 Db 313 -TGAATGCGGAGCCACAGTCTATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 371
 QY 777 CGCCCTTTCGCGCGGCGGCGGCTTCCACCGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCG 836
 Db 372 CCCCTTTCATCCAGCGG-----AGCGAATCCAAACCCCACTACCTACCTACCTACCTAC 422


```
QY 837 ACGAGATCGACCTGCCACCCACCATCTCGCTGTGACGCGGAGGAGCCCCACCCCTACC 896
Db      |||||
QY 423 ACGAAATGCGCTGCCACCCACCATCTCACTGTCTGATGGGGAGGAGCCCCACCCCTACC 482
Db      |||||
QY 897 AGGGCCCCCTGCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAAACCGGGAGT 956
Db      |||||
QY 483 AGGGCCCCCTGCACCCCTCCAGCTACGGGACCCCTGAGCAACAGCTGGAGCTGAACCGGGAAAT 542
Db      |||||
QY 957 CGGTGCGCGACCCCCCAACAGAAACATCTTCGACAGTGACCTGTGATGGATAGTGCCAGGC 1016
Db      |||||
QY 543 CTGTGCGCGCACCCCTTAACCGGACCATCTTCGACAGTGACCTTATAGACAGCACCATGC 602
Db      |||||
QY 1017 TGGGCGGCCCCCTGCCGCCCGCAGTAACCTCGGGCATCAGCGCCAGTGTCTACGGCAGCG 1076
Db      |||||
QY 603 TGGGGGGCCCCCTGTCCCCCGCAGCAGTAACCTCGGGCATCAGCGCCACCTGTCTACAGCAGCG 662
Db      |||||
QY 1077 GCGGGGCGCATGGAGGGGCGCGCCGCCACCTACAGCGAGGTCACTCGGCCACTACCCGGGGT 1136
Db      |||||
QY 663 GTGGGCGCATGGAGGGGCGCGCCGCCACCTACAGCGAGGTCACTCGGCCACTACCCCTGGCT 722
Db      |||||
QY 1137 CTTCTTCCAGCACACGACAGCAGTGCGGGCGCCCTCTCTTGTGTGGAGGGAGCCCGGCTCC 1196
Db      |||||
QY 723 CTTCTTCCAGCACACGACAGTAACGGGGCATCTCTCCCTGTCTAGAGGGAGCCCGGCTCC 782
Db      |||||
QY 1197 ACCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGATAAAC 1256
Db      |||||
QY 783 ATCACTCGCACATTGCCCCCACTGGA-----GAAACAAGGAGAGGAGAAAC 827
Db      |||||
QY 1257 AGAAAGGACACCTCTCTAGGGTCCCACAGGGGGCGG 1293
Db      |||||
QY 828 AGAAAGGTCAACCCCTCTAGGAGTGGGGGCCCGGGCG 864
Db      |||||
```

Search completed: February 19, 2005, 16:15:48
Job time : 4163.31 secs

This Page Blank (usprio)


```
QY 633 GCCGGCAGCAGCCAGGGCGGAGGAGAGATGCTCTGTCTCTCAGAGGATGCTGTGGC 692
Db 541 GCCGGCAGCAGCCAGGGCGGAGGAGAGATGCTCTGTCTCTCAGAGGATGCTGTGGC 600
QY 693 CTTGGAGAGCAGTGTACGAGCAACGAAATCCAGAGCGGAGGTTACGCCCGGCTC 752
Db 601 CTTGGAGAGCAGTGTACGAGCAACGAAATCCAGAGCGGAGGTTACGCCCGGCTC 660
QY 753 GGGCCACCGACCGCTGGCGGTGCGCCCTTCGCCAGCGGGAGCGCTTCCACGGCTTC 812
Db 661 GGGCCACCGACCGCTGGCGGTGCGCCCTTCGCCAGCGGGAGCGCTTCCACGGCTTC 720
QY 813 AGCCACCTATCTCGTACCTGCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTAG 872
Db 721 AGCCACCTATCTCGTACCTGCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTAG 780
QY 873 ACGGAGAGAGCCCGACCTTACAGGCGCCCTTGCACCTTCCAGCTTGGGAGCCCGGAGC 932
Db 781 ACGGAGAGAGCCCGACCTTACAGGCGCCCTTGCACCTTCCAGCTTGGGAGCCCGGAGC 840
QY 933 AGCAGCTGGAACCTGAACCGGGAGTCCGCTGCGCGCACCCCGACAGAACCTCTTCGACA 992
Db 841 AGCAGCTGGAACCTGAACCGGGAGTCCGCTGCGCGCACCCCGACAGAACCTCTTCGACA 900
QY 993 GTGACCTGTAGTGTAGTGGCGGCGGCGCCCTTGCACCTTCCAGCAGTAACTCGGGCA 1052
Db 901 GTGACCTGTAGTGTAGTGGCGGCGGCGCCCTTGCACCTTCCAGCAGTAACTCGGGCA 960
QY 1053 TCAGCGCAGCTGTACGAGCAGCGGCGGCGGAGTGGAGGCGCGCGCCCGACCTACAGCG 1112
Db 961 TCAGCGCAGCTGTACGAGCAGCGGCGGCGGAGTGGAGGCGCGCGCCCGACCTACAGCG 1020
QY 1113 AGTGTATCGGCACTACCGGGGTCTCTTCCAGCAGCAGCAGCAGTGGCGCGCCCT 1172
Db 1021 AGTGTATCGGCACTACCGGGGTCTCTTCCAGCAGCAGCAGCAGTGGCGCGCCCT 1080
QY 1173 CTTGTGTAGAGGAGCCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA 1232
Db 1081 CTTGTGTAGAGGAGCCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA 1140
QY 1233 TCTGAGCAAGAGAGAGTAAACAGAAAGGACACCTCTTAGGTGCTCCAGGGGGCC 1292
Db 1141 TCTGAGCAAGAGAGAGTAAACAGAAAGGACACCTCTTAGGTGCTCCAGGGGGCC 1200
QY 1293 GGGCTGGGCTGCTAGGTGAAAGGACAG 1321
Db 1201 GGGCTGGGCTGCTAGGTGAAAGGACAG 1229
```

RESULT 4

```
AX775889 1383 bp mRNA linear PAT 14-JUL-2003
LOCUS Sequence 159 from Patent WO03048202.
DEFINITION AX775889
```

```
ACCESSION AX775889
```

```
VERSION AX775889.1 GI:32693607
```

```
KEYWORDS
```

```
SOURCE Homo sapiens (human)
```

```
ORGANISM
```

```
Homo sapiens
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE
```

```
AUTHORS
```

```
TITLE
```

```
JOURNAL Patent: WO 03048202-A 159 12-JUN-2003;
```

```
Asahi Kasei Kabushiki Kaisha (JP)
```

```
FEATURES
```

```
source
```

```
1. .1383
```

```
/organism="Homo sapiens"
```

```
/mol_type="mRNA"
```

```
/db_xref="taxon:9606"
```

```
321. .1184
```

```
/note="unnamed protein product"
```

```
CDS
```

```
/codon_start=1
/protein_id="CAE11644.1"
/db_xref="GI:32693608"
/translation="MRLMGVNSTAAAGQNVNCTCNKESLQFOSMEITELFVQI
IIIVVMVNVVITCLSHYKLSARFISRHSGQRRRDLSDSSECLMPSLSTVSGN
GTEPQVYAPPRDRLAVPFAQRERFRFTYPLQHEIDLPTLISDGEERPP
YQPCITLQRPDPEQLELNRESVRAPPNRTIFSDLMSARLGGPCPPSSNGISATC
YSGGRMEGPPPTYSVIVGHYPGSPFHQSQSGPPSLLEGTRLHHTHIAPLSAAIWS
KEKQKQKHPL"
```

ORIGIN

```
Query Match 89.2%; Score 1178; DB 6; Length 1383;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 93 GGAAGCTAGCGGAGAGGCTCAGCCCCGGCGGAGCGCGCGCTGCCAGGCCCAT 152
Db 1 GGAAGCTAGCGGAGAGGCTCAGCCCCGGCGGAGCGCGCGCTGCCAGGCCCAT 60
QY 153 TTCCGAGACGCCACCGCGGGCAGCTGCCGACGCCCCCGGGGCTGCCAGGGAGCGCGGG 212
Db 61 TTCCGAGACGCCACCGCGGGGAGCTGCCGACGCCCCCGGGGCTGCCAGGGAGCGCGGG 120
QY 213 GGGCGCAGCGGAGCGCGTCCCGCAGCTGAGCCCCCGCGCGCCCCCGGGAACCTTGGCGGC 272
Db 121 GGGCGCAGCGGAGCGCGTCCCGCAGCTGAGCCCCCGCGCGCCCCCGGGAACCTTGGCGGC 180
QY 273 GACCGGAGCCCGGCGGAGCGGGCGCGCTCCCGCGCGCGCGCGCTTGCATGCGGGGC 332
Db 181 GACCGGAGCCCGGCGGAGCGGGCGCGCTCCCGCGCGCGCGCGCTTGCATGCGGGGC 240
QY 333 CCCAGCTCCGGCGCGCGCGGAGCGCCCCCGCGCGCGCCCCCGGAGCGCCCCCGCGCGCG 392
Db 241 CCCAGCTCCGGCGCGCGCGGAGCGCCCCCGCGCGCGCCCCCGGAGCGCCCCCGCGCG 300
QY 393 GCGCGCGCGCGCGCGCGTCCATGCAACCGCTTATGGGGGTCAACAGCACCGCGCGCGCG 452
Db 301 GCGCGCGCGCGCGCGCGTCCATGCAACCGCTTATGGGGGTCAACAGCACCGCGCGCGCG 360
QY 453 CGCGCGGCGAGCCCAATGCTCTCCAGCTGCAACTGCAAAACGCTTTGTTCAGAGCA 512
Db 361 CGCGCGGCGAGCCCAATGCTCTCCAGCTGCAACTGCAAAACGCTTTGTTCAGAGCA 420
QY 513 TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGATGA 572
Db 421 TGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGATGA 480
QY 573 TGGTGTGTGTATCAGTGTCTGTGAGCCACTAAGTGTGTGTGCACGGTTCCTTCATCA 632
Db 481 TGGTGTGTGTATCAGTGTCTGTGAGCCACTAAGTGTGTGTGCACGGTTCCTTCATCA 540
QY 633 GCGGCGCAGCGCGGGCGGAGGAGAGTGCCTGTCTCAGAGGATGCCTGTGGC 692
Db 541 GCGGCGCAGCGCGGGCGGAGGAGAGTGCCTGTCTCAGAGGATGCCTGTGGC 600
QY 693 CTTGGAGAGCAGTGTTCAGCAACCGGAATCCCGAGCGCGAGGTCTACGGCCCCCGCTC 752
Db 601 CTTGGAGAGCAGTGTTCAGCAACCGGAATCCCGAGCGCGAGGTCTACGGCCCCCGCTC 660
QY 753 GGGCCACCGACCGCTGGCGGTGCGCCCTTTCGCCAGCGGGAGCGCTTCCACGGTTC 812
Db 661 GGGCCACCGACCGCTGGCGGTGCGCCCTTTCGCCAGCGGGAGCGCTTCCACGGTTC 720
QY 813 AGCCACCTATCTCGTACCTGCAGCAGCAGATCGACTGCCACCCACCATCTCGCTGTAG 872
Db 721 AGCCACCTATCTCGTACCTGCAGCAGCAGATCGACTGCCACCCACCATCTCGCTGTAG 780
QY 873 ACGGGAGGAGCGCCCGACCTTACAGGGGCCCTTGACACCTTCCAGCTTGGGAGCCCGGAGC 932
Db 781 ACGGGAGGAGCGCCCGACCTTACAGGGGCCCTTGACACCTTCCAGCTTGGGAGCCCGGAGC 840
QY 933 AGCAGCTGGAACTGAACCGGGAGTCCGCTGCGCGCACCCCGACAGAACCTCTTCGACA 992
```


[illegible]

Db 644 CGTGCTACGACGCGCGCGCATGAGGGCGCGCCACCTACAGCGAGTCTATCG 703

Qy 1122 GCCACTACCGGGTCTCTCTTCAGACACAGCAGAGAGAGTGGGCCCTCTCTTGTGG 1181

Db 704 GCCACTACCGGGTCTCTCTTCAGACACAGCAGAGAGAGTGGGCCCTCTCTTGTGG 763

Qy 1182 AGGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 1241

Db 764 AGGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 823

Qy 1242 AAGAGAGAGTAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCGGGCTGGGG 1301

Db 824 AAGAGAGAGTAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCGGGCTGGGG 883

Qy 1302 CTGCTAGGTGAAGAGGAG 1321

Db 884 CTGCTAGGTGAAGAGGAG 903

RESULT 10

AR336831

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 759)

AUTHORS

SRIVASTAVA, S., MOUL, J.W., XU, L.L. and SEGAWA, T.

TITLE

Androgen-regulated gene expressed in prostate tissue

JOURNAL

Patent: US 6566130-A 2 20-MAY-2003;

FEATURES

Location/Qualifiers

1..759

source

organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 57.2%; Score 755; DB 6; Length 759;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 522 CGAGCTGGAGTTGTTTCAGATCATCATATCGGTGGTGTGATGATGATGATGATG 581

Db 5 CGAGCTGGAGTTGTTTCAGATCATCATATCGGTGGTGTGATGATGATGATGATG 64

Qy 582 TGATCAGTCTGCTGCTGAGCAGTCTGAGTGTCTGACCGTCTTTCATCAGCGGCGCA 641

Db 65 TGATCAGTCTGCTGCTGAGCAGTCTGAGTGTCTGACCGTCTTTCATCAGCGGCGCA 124

Qy 642 GCCAGGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAAGATGCTGTGGCCCTCGGAGA 701

Db 125 GCCAGGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAAGATGCTGTGGCCCTCGGAGA 184

Qy 702 GCACAGTGTGAGCAACCGGAATCCAGAGCGCAGGTCTACGCCCGCCCTCGGCCACCG 761

Db 185 GCACAGTGTGAGCAACCGGAATCCAGAGCGCAGGTCTACGCCCGCCCTCGGCCACCG 244

Qy 762 ACCGCTGGCGGTGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCAGGCCACCT 821

Db 245 ACCGCTGGCGGTGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCAGGCCACCT 304

Qy 822 ATCGTACCTGAGCAGAGATCGACTGCGCCACCGCATCTCTGCTCTCAGAGCGGGAGG 881

Db 305 ATCGTACCTGAGCAGAGATCGACTGCGCCACCGCATCTCTGCTCTCAGAGCGGGAGG 364

Qy 882 AGCCCCACCTTACAGGGGCCCTTGACCCCTTCCAGCTTCGGGACCCCGAGCAGAGTGG 941

Db 365 AGCCCCACCTTACAGGGGCCCTTGACCCCTTCCAGCTTCGGGACCCCGAGCAGAGTGG 424

Qy 942 AACTGAACCGGGAGTCTGGTGGCGCACCCCGCAACAGAACATCTTCGACAGTGAACCTGA 1001

Db 425 AACTGAACCGGGAGTCTGGTGGCGCACCCCGCAACAGAACCATCTTCGACAGTGAACCTGA 484

Qy 1002 TGATAGTGCAGGCTGGCGGCCCTGTGCCCGCCAGCAGTAACCTCGGGCATCAGCGCCA 1061

Db 485 TGATAGTGCAGGCTGGCGGCCCTGTGCCCGCCAGCAGTAACCTCGGGCATCAGCGCCA 544

Qy 1062 CGTGTACCGCAGCGGGCGGCATGAGGGGGCGCGCCACCTACAGCGAGTCTATCG 1121

Db 545 CGTGTACCGCAGCGGGCGGCATGAGGGGGCGCGCCACCTACAGCGAGTCTATCG 604

Qy 1122 GCCACTACCGGGTCTCTCTTCAGCACCAGCAGCAGTGGGCCCGCCCTCTCTTGTGG 1181

Db 605 GCCACTACCGGGTCTCTCTTCAGCACCAGCAGCAGTGGGCCCGCCCTCTCTTGTGG 664

Qy 1182 AGGGGACCGGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 1241

Db 665 AGGGGACCGGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 724

Qy 1242 AAGAGAGAGTAACAGAAAGGACACCTCTCTAG 1276

Db 725 AAGAGAGAGTAACAGAAAGGACACCTCTCTAG 759

RESULT 11

BD272494

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 969)

AUTHORS

BARNES, T.M., HOLTZMAN, D.A., SHARP, J.D. and FRASER, C.C.

TITLE

Secreted proteins and nucleic acids encoding them

JOURNAL

Patent: JP 2002539773-A 3 26-NOV-2002;

COMMENT

MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002539773-A/3

PD 26-NOV-2002 JP 2000602247

PF 01-MAR-2000 JP 2000602247

PR 01-MAR-1999 US 60/122458

PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER

PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC

PC G01N33/50, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC

Secreted proteins and nucleic acids encoding them FH key

Location/Qualifiers

FT CDS

(6)..(761).

Location/Qualifiers

1..969

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

FEATURES

source

Query Match 56.7%; Score 749; DB 6; Length 969;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 522 CGGAGCTGGAGTTGTTTCAGATCATCATCTCGTGGTGGTGTGATGATGATGATG 581

Db 10 CGGAGCTGGAGTTGTTTCAGATCATCATCTCGTGGTGGTGTGATGATGATGATG 69

Qy 582 TGATCAGTCTGCTGCTGAGCAGTCTACAGCTGTCTGACCGTCTTTCATCAGCGGCGCA 641

Db 70 TGATCAGTCTGCTGCTGAGCAGTCTACAGCTGTCTGACCGTCTTTCATCAGCGGCGCA 129

Qy 642 GCAGGGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGA 701

Db	130	GCCAGGGCGGAGGAGAGAGTGCCTGTCTCAGAAAGGATGCTGTGGCCCTCGGAGA	189
Qy	702	GCACAGTGTCAAGCAACGGAATCCAGAGCCGCAAGTCTTAGCCCCGCGCTCGGCCACCG	761
Db	190	GCACAGTGTCAAGCAACGGAATCCAGAGCCGCAAGTCTAGCCCCGCGCTCGGCCACCG	249
Qy	762	ACCGCCTGGCCGTGCGCGCCCTTCGCCCAAGCGGAGCGCTTCACGCGTTCAGGCCACCT	821
Db	250	ACCGCCTGGCCGTGCGCGCCCTTCGCCCAAGCGGAGCGCTTCACGCGTTCAGGCCACCT	309
Qy	822	ATCCGTACTCTGAGCACAGAGATGCAGCTGCCACCACCACATCTCGTGTTCAGACGGGGAGG	881
Db	310	ATCCGTACTCTGAGCACAGAGATGCAGCTGCCCGCCACCACATCTCGTGTTCAGACGGGGAGG	369
Qy	882	AGCCCCAACCTTACAGGGCCCCCTGCACTCTCAGCTTTCGGGAGCCCGAGCAGCAGCTGG	941
Db	370	AGCCCCAACCTTACAGGGCCCCCTGCACTCTCAGCTTTCGGGAGCCCGAGCAGCAGCTGG	429
Qy	942	AACATGAACGGGAGTCCGTGCGCGCACCCCAACAGAACATCTTTGCAAGTGAACCTGA	1001
Db	430	AACATGAACGGGAGTCCGTGCGCGCACCCCAACAGAACATCTTTGCAAGTGAACCTGA	489
Qy	1002	TGGATAGTGCAGGCTGGGGCGGCCCTTGCSCCCCCCAGCAGTAACCTCGGGCATCAGCGCCA	1061
Db	490	TGGATAGTGCAGGCTGGGGCGGCCCTTGCSCCCCCCAGCAGTAACCTCGGGCATCAGCGCCA	549
Qy	1062	CGTGCTACGGCAGCGGGCGGCGCATAGAGGGGCGCGCCCACTACAGCGAGTCAATCG	1121
Db	550	CGTGCTACGGCAGCGGGCGGCGCATAGAGGGGCGCGCCCACTACAGCGAGTCAATCG	609
Qy	1122	GCCACTACCGGGGTCTCTCTTCAGCACACAGCAGACAGTGGGCGCCCTCTTGCTGG	1181
Db	610	GCCACTACCGGGGTCTCTCTTCAGCACACAGCAGACAGTGGGCGCCCTCTTGCTGG	669
Qy	1182	AGGGGACCCGGTCCACCAACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGAGCA	1241
Db	670	AGGGGACCCGGTCCACCAACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGAGCA	729
Qy	1242	AAGAGAAGGATAACAGAAAGGACCCCTCTTAGGGTCCCAAGGGGGCGGGCTGGGG	1301
Db	730	AAGAGAAGGATAACAGAAAGGACCCCTCTTAGGGTCCCAAGGGGGCGGGCTGGGG	789
Qy	1302	CTCGTAGGTGAAAAGSCAG	1321
Db	790	CTCGTAGGTGAAAAGSCAG	809

```

RESULT 12
AX775887
LOCUS
AX775887      1085 bp      mRNA
DEFINITION
Sequence 157 from Patent WO03048202.
ACCESSION
AX775887
VERSION
AX775887.1  GI:32693605
KEYWORDS
.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
Matsuda, A. and Muramatsu, S.
AUTHORS
NF-kB activating gene
TITLE
Patent: WO 03048202-A 157 12-JUN-2003;
JOURNAL
Asahi Kasei Kabushiki Kaisha (JP)
FEATURES
Location/Qualifiers
1..1085
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
128..886
/note="unnamed protein product"
/codon_start=1
/protein_id="CAE11643.1"
/db_xref="GI:32693606"
CDS

```



```
Db 195 GTGTGAGCAACGAATCCAGAGCGCAGGTCTACGCGCCGCTCGGCCACCGACCGC 254
Qy 767 GTGCGGTGCGCGCTTTCGCGCCAGCGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 826
Db 255 CTGCGCGTGCCTTTCGCGCCAGCGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 314
Qy 827 TACCTGACGACGAGATCGACTCGCCTGCCACCCACCACTCTCGTGTGACAGCGGAGGAGCC 886
Db 315 TACCTGACGACGAGATCGACTCGCCTGCCACCCACCACTCTCGTGTGACAGCGGAGGAGCC 374
Qy 887 CCACCTTACAGGCGCGCTTTCGCGCCAGCGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 946
Db 375 CCACCTTACAGGCGCGCTTTCGCGCCAGCGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 434
Qy 947 AACCGGAGTGGTGGCGCGACCCCAACAGAACCACTCTCGACAGTGAACCTGATGGAT 1006
Db 435 AACCGGAGTGGTGGCGCGACCCCAACAGAACCACTCTCGACAGTGAACCTGATGGAT 494
Qy 1007 AGTCCAGGTGGCGCGCTTTCGCGCCAGCGAGTGAACCTCGGCGATCAGCGCCACCTGC 1066
Db 495 AGTCCAGGTGGCGCGCTTTCGCGCCAGCGAGTGAACCTCGGCGATCAGCGCCACCTGC 554
Qy 1067 TACGCGAGCGCGCGCTTTCGCGCCAGCGAGTGAACCTCGGCGATCAGCGCCACCTGC 1126
Db 555 TACGCGAGCGCGCGCTTTCGCGCCAGCGAGTGAACCTCGGCGATCAGCGCCACCTGC 614
Qy 1127 TACCGCGGTGCTCTCTTCCAGCACAGCAGAGTGGCGCGCTTCTGCTGGAGGG 1186
Db 615 TACCGCGGTGCTCTCTTCCAGCACAGCAGAGTGGCGCGCTTCTGCTGGAGGG 674
Qy 1187 ACCGCGTCCACCAACACACATCGCGCCCTAGAGAGCGAGCATCTGAGCAAAAGAG 1246
Db 675 ACCGCGTCCACCAACACACATCGCGCCCTAGAGAGCGAGCATCTGAGCAAAAGAG 734
Qy 1247 AAGGATAACAGAAAGACACCTCTCTAGGCTTCCAGCGGCGCGGCTGGGGTGGCG 1306
Db 735 AAGGATAACAGAAAGACACCTCTCTAGGCTTCCAGCGGCGCGGCTGGGGTGGCG 794
Qy 1307 TAGGTGAAAAGGCGAG 1321
Db 795 TAGGTGAAAAGGCGAG 809

RESULT 15
BD272545
LOCUS Secreted proteins and nucleic acids encoding them.
DEFINITION 759 bp DNA linear PAT 17-JUL-2003
ACCESSION BD272545
VERSION BD272545.1 GI:33082313
KEYWORDS JP 2002539773-A/54.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 759)
Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 54 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
EN JP 2002539773-A/54
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES,DOUGLAS A HOLTZMAN,JOHN D SHARP,CHRISTOPHER C
PI FRASER
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68,PC
GOIN33/15,
PC GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566,C12N15/00,C12N5/00,CC
Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers
FT source 1..759
```

```
FEATURES             FT            Location/Qualifiers
source               1..759
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"

ORIGIN
Query Match       53.3%; Score 704; DB 6; Length 759;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 754; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 522 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGAATGGTGAATGGTGG 581
Db 5 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGAATGGTGAATGGTGG 64
Qy 582 TGATCAGTGTCTGTGAGCCTACTCAAGTGTCTGACGGTCTTTCATCAGCGGAC 641
Db 65 TGATCAGTGTCTGTGAGCCTACTCAAGTGTCTGACGGTCTTTCATCAGCGGAC 124
Qy 642 GCCAGGCGGAGGAGAGAGATGCCCTGTCTCAGAAAGTGCCTGTGCGCCCTCGG 701
Db 125 GCCAGGCGGAGGAGAGAGATGCCCTGTCTCAGAAAGTGCCTGTGCGCCCTCGG 184
Qy 702 GCACAGTGTGAGCAACGGAATCCAGAGCGCGAGGTCTACGCGCCGCTCGGCC 761
Db 185 GCACAGTGTGAGCAACGGAATCCAGAGCGCGAGGTCTACGCGCCGCTCGGCC 244
Qy 762 ACCGCTTGGCGTGGCGCCCTTTCGCGCCAGCGGAGCGCTTTCACCGCTTTCAG 821
Db 245 ACCGCTTGGCGTGGCGCCCTTTCGCGCCAGCGGAGCGCTTTCACCGCTTTCAG 304
Qy 822 ATCCGTACCTGAGCAGCAGAGTGCCTGCGCCACCACTCTCGTGTGAGCGGGAG 881
Db 305 ATCCGTACCTGAGCAGCAGAGTGCCTGCGCCACCACTCTCGTGTGAGCGGGAG 364
Qy 882 AGCCCCCACCCTTACAGGGCCCTTGCACCTTCCAGCTTCCGAGACCCGAGCAGCT 941
Db 365 AGCCCCCACCCTTACAGGGCCCTTGCACCTTCCAGCTTCCGAGACCCGAGCAGCT 424
Qy 942 AACTGAAACCGGAGTGGTGGCGGACCCCAACCAACCAACCAACCAACCAACCA 1001
Db 425 AACTGAAACCGGAGTGGTGGCGGACCCCAACCAACCAACCAACCAACCAACCA 484
Qy 1002 TGGATAGTCCAGGCTGGCGCGCCCTGCGCCCGCCAGCAGTAACCTCGGGCATC 1061
Db 485 TGGATAGTCCAGGCTGGCGCGCCCTGCGCCCGCCAGCAGTAACCTCGGGCATC 544
Qy 1062 CBTGTACGCGCAGCGCGCGCATGAGGGCGCGCGCCACCTACAGCAGGTCATCG 1121
Db 545 CBTGTACGCGCAGCGCGCGCATGAGGGCGCGCGCCACCTACAGCAGGTCATCG 604
Qy 1122 GCACTTACCGGGTCTCTTTCAGCACCAGCAGCAGTGGCGCGCCCTCTTCTGCT 1181
Db 605 GCACTTACCGGGTCTCTTTCAGCACCAGCAGCAGTGGCGCGCCCTCTTCTGCT 664
Qy 1182 AGGGACCCCGGTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAG 1241
Db 665 AGGGACCCCGGTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAG 724
Qy 1242 AAGAGAAGGATAAACAGAAAGGACACCTCTCTAG 1276
Db 725 AAGAGAAGGATAAACAGAAAGGACACCTCTCTAG 759
```

Search completed: February 19, 2005, 22:03:56
Job time : 5702.7 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 16:16:01 ; Search time 707.116 Seconds
(without alignments)
11058.969 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcgagcgca.....ctgcgtaggtgaaagcgag 1321

Scoring table:
OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	6	ABK12137 Human cDN
2	1301	98.5	4911	13	ACN40804
3	1229	93.0	4839	8	ACC49552 Tumour-as
4	1229	93.0	4839	11	ADP65809 Human STA
5	1229	93.0	4839	11	ADP65729 Human tra
6	1229	93.0	4839	12	ADM67045 Human hom
7	1229	93.0	4839	13	ADR65875 Human pro
8	1229	93.0	4839	13	ADR66778 Human pro
9	1178	89.2	1383	10	ADC37326 Nuclear f
10	864	65.4	864	11	ADN38809 Cancer/an
11	800	60.6	1140	6	ABK92120 Prostate
12	800	60.6	1140	10	AAD60105 Human and
13	800	60.6	1140	10	ADH62276 Human PME
14	800	60.6	1140	12	ADO39826 Human PME
15	800	60.6	1141	10	ADB75588 Prostate
16	800	60.6	1850	8	ACC49536 Tumour-as
17	800	60.6	4527	11	ADL83313 Human and
18	788	59.7	1066	4	AAI57868 Human pol
19	755	57.2	759	10	ADF17545 Human and
20	755	57.2	759	10	ADH62277 Human PME

21	755	57.2	759	12	ADO39827
22	749	56.7	969	3	AAA75151
23	749	56.7	1061	3	AAA47429
24	749	56.7	1085	10	ADC37324
25	749	56.7	1334	8	ABZ36103
26	744	56.3	969	3	AAA75163
27	713	54.0	806	8	ACC49537
28	698	52.8	969	3	AAA75164
29	698	52.8	969	3	AAA75165
30	560	42.4	1583	6	ABS61424
C 31	409	31.0	711	12	ADO00336
C 32	409	31.0	711	12	ADN98767
C 33	401	30.4	408	5	AAF65983
C 34	394	29.8	1089	4	AAI59654
C 35	364	27.6	474	10	ABZ84732
C 36	302	22.9	693	6	ABK12143
C 37	271	20.5	812	2	AAZ52964
C 38	229	17.3	254	3	AAA41265
C 39	178	13.5	467	9	ACH14862
C 40	106	8.0	1879	5	AAS84503
C 41	63	4.8	426	5	AAS84502
C 42	60	4.5	60	6	ABN40872
C 43	56	4.2	522	6	ABT10027
C 44	51	3.9	51	4	AAH89714
C 45	45	3.4	837	6	ABQ43501

ALIGNMENTS

RESULT 1
ABK12137
ID ABK12137 standard; cDNA; 1321 BP.
XX
AC ABK12137;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
XX
KW Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
KW cytosolic; cadiant; cerebroprotective; antiarteriosclerotic;
KW cardiac cell; anti-apoptotic; vascular endothelial cell;
KW cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
KW heart failure.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 413..1276
FT /*tag= a
FT /product= "MIVR-1"
FT /note= "This region is specifically claimed in claim 3"
XX
WO200216416-A2.
XX
28-FEB-2002.
XX
21-AUG-2001; 2001WO-US026089.
XX
22-AUG-2000; 2000US-0227159P.
XX
(BGMH) BRIGHAM & WOMENS HOSPITAL INC.
(PFIZ) PFIZER INC.
XX
Lee RT, Landschulz KT, Kennedy SP, Thompson JF, Turi TG;
XX
WPI; 2002-280912/32.
XX
P-PSDB; AAU78231.
XX
Novel nucleic acid molecule encoding Mechanically Induced Vascular
XX
Receptor-1 polypeptide, useful for treating cardiovascular diseases.

Claim 2: Page 87-88; 105pp: English.

The invention relates to an isolated nucleic acid molecule encoding a Mechanically induced vascular receptor (MIVR)-1 polypeptide having cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences AI761441.1, A1594390, NM 004338 and AQ17461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, a candidate molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IEX-1, VDP-1, BTG-2 and TIS-11d or its expression product, determining if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and disorders as characterised by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart failure. The present sequence encodes human MIVR-1

Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

SQ Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1321;	DB 6;	Length 1321;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 1321;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CGACCGGGGTCTCGAGCGAAACCCGATCTCTCTTGGACTTCGAATCAGAGGAGGAGGCGG	60	
Db	1	CGACCGGGGTCTCGAGCGAAACCCGATCTCTCTTGGACTTCGAATCAGAGGAGGAGGCGG	60	
Qy	61	CGGCGGGCGGGCGGAGGCGCTCGCTCGGGGAAAGCTAGCGGCAGAGGCTCAGCCCC	120	
Db	61	CGGCGGGCGGGCGGAGGCGCTCGCTCGGGGAAAGCTAGCGGCAGAGGCTCAGCCCC	120	
Qy	121	GGGGGACGCGCGCGCCCGCTGTCAGACCCATTTTCGAGACGCCACCCCGCGGGGACCTGGCG	180	
Db	121	GGGGGACGCGCGCGCCCGCTGTCAGACCCATTTTCGAGACGCCACCCCGCGGGGACCTGGCG	180	
Qy	181	ACGCCCCCGGGGCTGCCAGAGGGAGGCCGGGGGGCGGCGAGCGGAGCGCGTCCGCGGCAC	240	
Db	181	ACGCCCCCGGGGCTGCCAGAGGGAGGCCGGGGGGCGGCGAGCGGAGCGCGTCCGCGGCAC	240	
Qy	241	TGAGCCCCCGGGCGCCCCCGGGAACTTGCGGGCGACCCCGAGGCCCGGGCGGGGCGGCGC	300	
Db	241	TGAGCCCCCGGGCGCCCCCGGGAACTTGCGGGCGACCCCGAGGCCCGGGCGGGGCGGCGC	300	
Qy	301	CTCCCCCGCGCGGCGCTCTCTGATCGGGGGCCCGAGCTCGGGGGCGCGCGGAGCCCCC	360	
Db	301	CTCCCCCGCGCGGCGCTCTCTGATCGGGGGCCCGAGCTCGGGGGCGCGCGGAGCCCCC	360	
Qy	361	CCCCGGGCGCCCCGAGCCCCCGCGCCCCCGCGCGCGCGCGCGCGCTCCATGCACCG	420	
Db	361	CCCCGGGCGCCCCGAGCCCCCGCGCCCCCGCGCGCGCGCGCGCGCTCCATGCACCG	420	
Qy	421	CTTGATGGGGGTCAACGACACCGCGCGCGCGCGCGCGGGGAGGCCCAATGTCTCTGTCAC	480	
Db	421	CTTGATGGGGGTCAACGACACCGCGCGCGCGCGCGCGGGGAGGCCCAATGTCTCTGTCAC	480	
Qy	481	GTGCAACTGCAAAACGCTTTTGTTCACAGACATGAGAGATCGAGAGCTGGAGTTTGTTC	540	
Db	481	GTGCAACTGCAAAACGCTTTTGTTCACAGAGATGAGAGATCGAGAGCTGGAGTTTGTTC	540	
Qy	541	GATCATCATCATCGTGGTGGTGATGCTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	600	
Db	541	GATCATCATCATCGTGGTGGTGATGCTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	600	
Qy	601	CCACTACAAGCTGTCTGACGGTCTTTTCATCAGCGGGCAAGCCAGGGGCGGAGGAGAGA	660	
Db	601	CCACTACAAGCTGTCTGACGGTCTTTTCATCAGCGGGCAAGCCAGGGGCGGAGGAGAGA	660	
Qy	661	AGATGCCCTGTCCTCAGAGGATGCTGTGGCCCTCGGAGAGCACAGTGTCAAGGCAACGG	720	
Db	661	AGATGCCCTGTCCTCAGAGGATGCTGTGGCCCTCGGAGAGCACAGTGTCAAGGCAACGG	720	


```
PA (GETH ) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
XX WPI; 2004-347921/32.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 1; SEQ ID NO 5823; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acids and
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment of
XX cancer in mammals. TAT polypeptides, nucleic acids,
XX antibodies, antagonists, binding molecules and compositions are useful
XX for diagnosing or treating a cell proliferative disorder associated with
XX increased TAT expression, particularly cancers such as breast cancer,
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX cancer, pancreatic cancer, cervical cancer, cancers of the central
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
XX used as hybridisation probes, in chromosome and gene mapping, in
XX chromosome identification and in gene therapy. The present sequence
XX represents a TAT nucleic acid of the invention
XX
SQ Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;

Query Match          98.5%; Score 1301; DB 13; Length 4911;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AACCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGCGCGCGGCGGCGGCGGAG 80
DB 1 AACCCGATCTCCTTGGACTTGAATGAGGAGGAGGAGCGCGCGGCGGCGGCGGAG 60
QY 81 GCGCTCGGCTGGGAAAGCTAGCGGCGAGAGGCTCAGCCCGCGGCGGCGGCGGCGG 140
DB 61 GCGCTCGGCTGGGAAAGCTAGCGGCGAGAGGCTCAGCCCGCGGCGGCGGCGGCGG 120
QY 141 TGGCAGGCCATTTTCGGAGCGCCACCGCGGCGGAGCTGCGGAGCGGCGGCGGCGG 200
DB 121 TGGCAGGCCATTTTCGGAGCGCCACCGCGGCGGAGCTGCGGAGCGGCGGCGGCGG 180
QY 201 GGGAGGCGGCGGCGGCGGAGCGGCTGCGGCGGAGCTGAGCGGCGGCGGCGGCGG 260
DB 181 GGGAGGCGGCGGCGGCGGAGCGGCTGCGGCGGAGCTGAGCGGCGGCGGCGGCGG 240
QY 261 GAATCTGGCGGCGGAGCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
DB 241 GAATCTGGCGGCGGAGCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 321 TGCATGCGGCGGCGGCGGAGCTCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGG 380
DB 301 TGCATGCGGCGGCGGCGGAGCTCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGG 360
QY 381 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
DB 361 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 441 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 500
DB 421 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 501 TGTTCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTG 560
```

RESULT 3

ACC49552

ID ACC49552 standard; cDNA; 4839 BP.

XX ACC49552;

XX 01-JUL-2003 (first entry)

XX Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.

XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;

XX cancer; gene; ss.

XX Homo sapiens.

XX WO2003024392-A2.

XX

QY 1233 TCTGGAGCAAGAGAGTAACAGAAAGAGACACCTCTCTAGGTCCTCCCGGGGGCC 1292
DB 1141 TCTGGAGCAAGAGAGTAACAGAAAGAGACACCTCTCTAGGTCCTCCCGGGGGCC 1200
QY 1293 GGGCTGGGGCTGGCTAGGTGAAAGGCGAG 1321
DB 1201 GGGCTGGGGCTGGCTAGGTGAAAGGCGAG 1229

RESULT 6

ADM67045

ID ADM67045 standard; DNA; 4839 BP.

AC ADM67045;

DT 03-JUN-2004 (first entry)

XX Human homologue of murine adipocyte specific DNA SeqID 180.

XX human; adipocyte specific; ds; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW anti-diabetic; hypotensive.

XX Homo sapiens.

XX WO2004011618-A2.

XX 05-FEB-2004.

XX 29-JUL-2003; 2003WO-US023684.

XX 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

XX (HMGE-) HMGENCE INC.

XX Chada K, Chouinard R, Ashar H, Sayed AMD;

PI WPI; 2004-143846/14.

XX Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.

XX Claim 11; SEQ ID NO 180; 91pp; English.

XX This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C +/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, anti-diabetic and
CC hypotensive activities. This polynucleotide sequence is a human homologue
CC of a murine adipocyte specific DNA sequence of the invention.

SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.08; Score 1229; DB 12; Length 4839;

Best Local Similarity 100.0%; Pred. NO. 0;

Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGCGAGCGCGCCCGCTGCGACGCCAATT 152
DB 1 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGCGAGCGCGCCCGCTGCGACGCCAATT 60
QY 153 TTCCGACACGACCCCGCGGCGACTGCGCGAGCGCCCGCGGCGCTCCGAGGGAGGCGCGGG 212
DB 61 TTCCGAGCGCCACCGCGGCGACTGCGCGAGCGCCCGCGGCGCTCCGAGGGAGGCGCGGG 120
QY 213 GGGCGAGCGGAGCGCGGCTCCCGGCACTGAGCGCCCGCGGCGCCCGGGAACTTGGCGGC 272
DB 121 GGGCGAGCGGAGCGCGGCTCCCGCACTGAGCGCCCGCGGCGCCCGGGAACTTGGCGGC 180
QY 273 GACCCGAGCGCGGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTTCTGTCATGCGGGGC 332
DB 181 GACCCGAGCGCGGAGCGCGGCGCGCTTCCCGCGCGCGCGCTTCTGTCATGCGGGGC 240
QY 333 CCAGGCTCCGGGCGCGGCGGAGCGCCCGCGCGCGCGCCCGCGGCGCCCGCGC 392
DB 241 CCAGGCTCCGGGCGCGGCGGAGCGCCCGCGCGCGCGCCCGCGGCGCCCGCGC 300
QY 393 GCCGCGCGCGCGCGCTGTCATGCAACGCTTGTGATGGGGTCAACAGACACCGCGCGCGC 452
DB 301 GCCGCGCGCGCGCGCTGTCATGCAACGCTTGTGATGGGGTCAACAGACACCGCGCGCGC 360
QY 453 CGCGCGGCGAGCGCCCAATGCTCTCTGCACTGCAACTGCAACGCTCTTGTTCAGAGCA 512
DB 361 CGCGCGGCGAGCGCCCAATGCTCTCTGCACTGCAACTGCAACGCTCTTGTTCAGAGCA 420
QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCTGCTGGTGGTGTATGATGATGA 572
DB 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCTGCTGGTGGTGTATGATGATGA 480
QY 573 TGGTGGTGGTGTACGTGCTGAGCGCTGCTGAGCCACTACAAGCTGTCTGCAAGTCTTCTATCA 632
DB 481 TGGTGGTGGTGTACGTGCTGAGCGCTGCTGAGCGCTGCTGCAAGTGTCTGCAAGTCTTCTATCA 540
QY 633 GCCGCGACAGCGCGGCGGAGAGAGATGCTGCTGCTCAGAGGATGCTGTGGC 692
DB 541 GCCGCGACAGCGCGGCGGAGAGAGATGCTGCTGCTCAGAGGATGCTGTGGC 600
QY 693 CTTGCGAGAGCACAGTGTGAGCAACGGAATCCAGAGCGCGAGTCTACGCCCGCGCTC 752
DB 601 CTTGCGAGAGCACAGTGTGAGCAACGGAATCCAGAGCGCGAGTCTACGCCCGCGCTC 660
QY 753 GGGCCACCGACCGCTGGCGCTGCGCGCTTCCGCCAGCGGAGCGCTTCCACCGCTTC 812
DB 661 GGGCCACCGACCGCTGGCGCTGCGCGCTTCCGCCAGCGGAGCGCTTCCACCGCTTC 720
QY 813 AGCCCACTATTCGTACCTGCGAGCAGAGATCGACCTGCCACCCACCATCTCGTGTGAG 872
DB 721 AGCCCACTATTCGTACCTGCGAGCAGAGATCGACCTGCCACCCACCATCTCGTGTGAG 780
QY 873 AGGGGAGGAGCGCCCGACCCCTACAGGCGCCCTGCAAGTCTTCCAGCTTCCGAGCGCG 932
DB 781 AGGGGAGGAGCGCCCGACCCCTACAGGCGCCCTGCAAGTCTTCCAGCTTCCGAGCGCG 840
QY 933 AGCAGCTGGAACCTGAACCGGGAGTCTGGTGGCGCGACCCCGCAACAGAACCATCTTCGACA 992
DB 841 AGCAGCTGGAACCTGAACCGGGAGTCTGGTGGCGCGACCCCGCAACAGAACCATCTTCGACA 900
QY 993 GTGACCTGATGAGTGTGCGAGGCTGGGGGGCGCTTGGCGCGCGCGCGCGCGCGCGCGCA 1052
DB 901 GTGACCTGATGAGTGTGCGAGGCTGGGGGGCGCTTGGCGCGCGCGCGCGCGCGCGCGCA 960
QY 1053 TCAGCGCGCGCTGCTACGCGCGGCGGCGATGAGGGGGCGCGCGCGCGCGCGCGCGCGCG 1112
DB 961 TCAGCGCGCGCTGCTACGCGCGGCGGCGATGAGGGGGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1113 AGGTCTATCGGCGCACTACCGGGGTCTCTTCCAGCACAGAGAGAGAGAGAGAGAGAGAGAG 1172
DB 1021 AGGTCTATCGGCGCACTACCGGGGTCTCTTCCAGCACAGAGAGAGAGAGAGAGAGAGAGAG 1080

QY 713 GGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCGGCCACCGACCGCTGGCC 772
Db 301 GGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCGGCCACCGACCGCTGGCC 360
QY 773 GTGCGCGCTTCGCGCGAGGGAGCGTTCACCGCTTCAGCGCCACCTATCGGTACTG 832
Db 361 GTGCGCGCTTCGCGCGAGGGAGCGTTCACCGCTTCAGCGCCACCTATCGGTACTG 420
QY 833 CAGCAGAGATCGACCTGCGCACCCACCATCTCGGTGTCAGACGGGAGGACCCACCC 892
Db 421 CAGCAGAGATCGACCTGCGCACCCACCATCTCGGTGTCAGACGGGAGGACCCACCC 480
QY 893 TACCAGGCGCTTCACCTTCAGCTTCGGGACCCCGAGCAGCGCTGGAACCTGAACCGG 952
Db 481 TACCAGGCGCTTCACCTTCAGCTTCGGGACCCCGAGCAGCGCTGGAACCTGAACCGG 540
QY 953 GAGTCGCTGCGCGACCCCAACAGAACCATCTTCAGAGTGACCTGATGATGATGCGC 1012
Db 541 GAGTCGCTGCGCGACCCCAACAGAACCATCTTCAGAGTGACCTGATGATGATGCGC 600
QY 1013 AGGTCGCGCGCTTCGCGCGACCCCGAGCAGCGCTGGAACCTGAACCTGAACCGG 1072
Db 601 AGGTCGCGCGCTTCGCGCGACCCCGAGCAGCGCTGGAACCTGAACCTGAACCGG 660
QY 1073 AGGTCGCGCGCTTCGCGCGACCCCGAGCAGCGCTGGAACCTGAACCTGAACCGG 1132
Db 661 AGGTCGCGCGCTTCGCGCGACCCCGAGCAGCGCTGGAACCTGAACCTGAACCGG 720
QY 1133 GGGTCCTCTTCAGCAGCAGCAGCAGTGGGCGCGCTTCGTCGAGGGGACCGG 1192
Db 721 GGGTCCTCTTCAGCAGCAGCAGCAGTGGGCGCGCTTCGTCGAGGGGACCGG 780
QY 1193 CTCACACACACACATCGCGCGCTTCAGAGCGCAGCGCTTCGAGCAAGAGAGGAT 1252
Db 781 CTCACACACACACATCGCGCGCTTCAGAGCGCAGCGCTTCGAGCAAGAGAGGAT 840
QY 1253 AATCAGAAAGGACACCTCTCTAG 1276
Db 841 AATCAGAAAGGACACCTCTCTAG 864

RESULT 11

ABK92120
ID ABK92120 standard; DNA; 1140 BP.

XX AC ABK92120;

XX DT 15-AUG-2002 (first entry)

XX DE Prostate cancer-associated DNA sequence #6.

XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

XX KW gene therapy; gene; ds.

XX OS Mammalia.

XX PN WO200230268-A2.

XX PD 18-APR-2002.

XX PF 12-OCT-2001; 2001WO-US032045.

XX PR 13-OCT-2000; 2000US-00687576.

XX PR 08-DEC-2000; 2000US-00733288.

XX PR 08-DEC-2000; 2000US-00733742.

XX PR 24-JAN-2001; 2001US-0263957P.

XX PR 16-MAR-2001; 2001US-0276791P.

XX PR 16-MAR-2001; 2001US-0276888P.

XX PR 06-APR-2001; 2001US-0286214P.

XX PR 30-APR-2001; 2001US-00847046.

XX PR 04-MAY-2001; 2001US-0288589P.

XX (SOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

XX WPI; 2002-471335/50.
P-PSDB; ABG61805.

DR Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.

XX Claim 22; Page 305; 436pp; English.

XX The present invention relates to methods of detecting a prostate cancer-
XX associated transcript in a cell from a patient. The method comprises
XX contacting a biological sample from the patient with prostate cancer-
XX associated polynucleotides (designated PC genes) that selectively
XX hybridise to a sequence that is at least 80% identical to them. The
XX prostate cancer-associated polynucleotide sequences are differentially
XX expressed in prostate tumour tissue or in prostate cancer and are derived
XX from the tissues of various organisms such as humans or other mammals
XX (e.g. mice, sheep and dogs). The methods of the invention are useful for
XX diagnosing and treating prostate cancer in mammals. The prostate cancer-
XX associated genes are useful for diagnosing or treating prostate cancer,
XX as well as for identifying modulators of prostate cancer or agents that
XX inhibit prostate cancer. The nucleic acid sequences are particularly
XX useful in gene therapy, as a vaccine or in antisense applications.

XX ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
XX sequences

XX SQ Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

Query Match 60.6%; Score 800; DB 6; Length 1140;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGG 581

Db 100 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGG 159

QY 582 TGATCAGTGGCTGTGAGCCACTAAGCTGTCTGACGGTCTTTCATCAGCCGACCA 641

Db 160 TGATCAGTGGCTGTGAGCCACTAAGCTGTCTGACGGTCTTTCATCAGCCGACCA 219

QY 642 GCCAGGGCGGAGGAGAGATGCCCTGCTTCAGAGGATGCCCTGTGGCCTCGGAG 701

Db 220 GCCAGGGCGGAGGAGAGATGCCCTGCTTCAGAGGATGCCCTGTGGCCTCGGAG 279

QY 702 GCACAGTGTGAGGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCGGCCACCG 761

Db 280 GCACAGTGTGAGGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCGGCCACCG 339

QY 762 ACCGCTGGCCGTGCGCCCTTTCGCGCAGCGGGAGCGCTTCCACCGCTTCCAGCCACT 821

Db 340 ACCGCTGGCCGTGCGCCCTTTCGCGCAGCGGGAGCGCTTCCACCGCTTCCAGCCACT 399

QY 822 ATCCGCTACCTGAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTGAGCGGGAGG 881

Db 400 ATCCGCTACCTGAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTGAGCGGGAGG 459

QY 882 AGCCCCCACCCTTACAGGGGCCCTTCGACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGG 941

Db 460 AGCCCCCACCCTTACAGGGGCCCTTCGACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGG 519

QY 942 AACTGAAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCGACATGACCTGA 1001

Db 520 AACTGAAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCGACATGACCTGA 579

QY 1002 TGGATAGTGCAGGCTGGGCGGCCCTTCGCCCGCCCGAGAGTAACCTCGGCGCATCAGGCCCA 1061

Db 580 TGGATAGTGCAGGCTGGGCGGCCCTTCGCCCGCCCGAGAGTAACCTCGGCGCATCAGGCCCA 639

Qy	1062	CTGTCTACGGCAGCGGGGGCGCATGAGGGGCGCGCCCACTTACAGCGAGGTCATCG	1121
Db	640	CTGTCTACGGCAGCGGGGGCGCATGAGGGGCGCGCCCACTTACAGCGAGGTCATCG	699
Qy	1122	GCCACTACCCGGGGTCTCTCTTCAGACACAGACAGACAGTGGGCGCCCTCTCTTGTCTGG	1181
Db	700	GCCACTACCCGGGGTCTCTCTTCAGACACAGACAGACAGTGGGCGCCCTCTTGTCTGG	759
Qy	1182	AGGGGACCCGGCTCCACACACACATCTGGCGCCCTTAGAGAGCGCAGCCATCTTGAGACA	1241
Db	760	AGGGGACCCGGCTCCACACACACATCTGGCGCCCTTAGAGAGCGCAGCCATCTTGAGACA	819
Qy	1242	AAGAGAAGGATAACAGAAAGGACACCCCTCTTAGGGTCCCCAGGGGGGGCGGGCTGGGG	1301
Db	820	AAGAGAAGGATAACAGAAAGGACACCCCTCTTAGGGTCCCCAGGGGGGGCGGGCTGGGG	879
Qy	1302	CTCGTAGGTGAAAGGCAG	1321
Db	880	CTCGTAGGTGAAAGGCAG	899

RESULT 12

AAD60105
ID AAD60105 standard: cDNA: 1140 BP.

AA AAD60105:

AA	
DT	18-DEC-2003 (first entry)

DE Human androgen-regulated gene (ARG), PMEPA1.

Human; androgen-regulated gene; ARG; PMEPA1; prostate cancer; KW

KW chromosome 20q13; gene; ss.

XX
OS Homo sapiens.

Key	Location/Qualifiers
CDS	95. .853

```
FT
/*tag= a
```

FT /product= "Human PMEPA1 protein"

FT /note= "CDS is referred to as SEQ ID NO:2 in claim 1 of
FT the specification"

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

PN US6566130-B1.

XX
PD 20-MAY-2003.

26-JAN-2001; 2001US-00769482.

XX
PR 28-JAN-2000; 2000US-0178772P.

PR 31-JAN-2000; 2000US-0179045P.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI Srivastava S, Moul JW, Xu LL, Segawa T;

DR WPI; 2003-719644/68.

DR P-PSDB; AAE39589.

Novel isolated androgen-regulated gene designated as PMEPA1 useful for selecting primers and probes for detecting prostate cancer cells in biological samples by nucleic acid amplification techniques.

PS Example 7; Col 29-30; 58pp; English.

CC The invention relates to an isolated androgen-regulated gene (ARG)
CC designated as PMPAL. The invention is useful for selecting primers and
CC probes for detecting prostate cancer cells in a biological sample by
CC using nucleic acid amplification techniques. The present sequence is,
CC human PMPAL cDNA, PMPAL gene chromosome 20q13

SQ Sequence 1140 BP; 271 A; 349 C; 336 G; 184 T; 0 U; 0 Other;

Query Match	60.6%;	Score 800;	DB 10;	Length 1140;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 800;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	522	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGGTGATGATGCTGATCGTGTGGTGG	581	
Db	99	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGGTGATGATGCTGATGATGCTGCTGG	158	
Qy	582	TGATCATCGTGCCTGTGAGCCACTAAGAAGTGTCTGACGGTCTCTTCAATCAGCCGGCACA	641	
Db	159	TGATCATCGTGCCTGTGAGCCACTAAGAAGTGTCTGACGGTCTCTTCAATCAGCCGGCACA	218	
Qy	642	GCCAGGGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGCCCTGTGCGCCCTCGGAGA	701	
Db	219	GCCAGGGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGCCCTGTGCGCCCTCGGAGA	278	
Qy	702	GCACAGTGTTCAGGCAACGGGAATCCACAGACCGCAGAGTCTACAGCCCGCCCTCGGCCACCG	761	
Db	279	GCACAGTGTTCAGGCAACGGGAATCCACAGACCGCAGAGTCTACAGCCCGCCCTCGGCCACCG	338	
Qy	762	ACCGCTTGGCCGTGCGCCCTTTCGCCACAGCGGAGCGCTTTCACACCGCTTTCAGCCCACT	821	
Db	339	ACCGCTTGGCCGTGCGCCCTTTCGCCACAGCGGAGCGCTTTCACACCGCTTTCAGCCCACT	398	
Qy	822	ATCCGTACCTGCAGCAGAGATCGACTCGCCACCCACCATCTCGCTGTCTAGACGGGGAGG	881	
Db	399	ATCCGTACCTGCAGCAGAGATCGACTCGCCACCCACCATCTCGCTGTCTAGACGGGGAGG	458	
Qy	882	AGCCCCACCTACACAGGGGCCCTTGCAACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGG	941	
Db	459	AGCCCCACCTACACAGGGGCCCTTGCAACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGG	518	
Qy	942	AACTGAACCGGGAGTCEGTGCGGCGACCCGCCAAGAACCATCTTTCGACAGTGACTGA	1001	
Db	519	AACTGAACCGGGAGTCEGTGCGGCGACCCGCCAAGAACCATCTTTCGACAGTGACTGA	578	
Qy	1002	TGGATAGTCCAGGCTGGGCGGCCCTTGCCGCCCCAGCAGTAACTCGGGCATCAGCGCCA	1061	
Db	579	TGGATAGTCCAGGCTGGGCGGCCCTTGCCGCCCCAGCAGTAACTCGGGCATCAGCGCCA	638	
Qy	1062	CGTGCTACGCGCAGCGCGGCGCATGAGAGGGCGCGCCCACTACAGCAGGTCAATCG	1121	
Db	639	CGTGCTACGCGCAGCGCGGCGCATGAGAGGGCGCGCCCACTACAGCAGGTCAATCG	698	
Qy	1122	GCACATACCGGGGTCTCTCTTCAGACACAGCAGCAGTGGGCGCCCTCTCTTGTCTGG	1181	
Db	699	GCACATACCGGGGTCTCTCTTCAGACACAGCAGCAGTGGGCGCCCTCTCTTGTCTGG	758	
Qy	1182	AGGGGACCGGGTCTCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA	1241	
Db	759	AGGGGACCGGGTCTCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA	818	
Qy	1242	AAGAGAAGGATAAACAGAAAGGACACCTCTCTTAGGGTCCCCAGGGGGCGCGGTGGGG	1301	
Db	819	AAGAGAAGGATAAACAGAAAGGACACCTCTCTTAGGGTCCCCAGGGGGCGCGGTGGGG	878	
Qy	1302	CTGCGTAGGTGAAAGGCAG 1321		
Db	879	CTGCGTAGGTGAAAGGCAG 898		
RESULT 13				
ADH62276				
ID	ADH62276 standard; cDNA; 1140 BP.			
XX	ADH62276;			
XX	25-MAR-2004 (first entry)			
DT	Human PMEPA1 cDNA.			
XX	Androgen-regulated gene; ARG; PMEPA1; therapy; diagnosis; prognosis;			
XX				

Androgen-regulated gene; ARG; PMEPA1; therapy; diagnosis; prognosis;

prostate cancer; hormonal therapy; human; chromosome 20q13; gene; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 95..853
/tag= a
/product= "Human PMEPA1 protein"
exon 96..263
/tag= b
exon 264..343
/tag= c
exon 344..853
/tag= d
intron 854..1134
/tag= e

US2003170713-A1.

11-SEP-2003.

18-MAR-2003; 2003US-00390045.

28-JAN-2000; 2000US-0178772P.

31-JAN-2000; 2000US-0179045P.

26-JAN-2001; 2001US-00769482.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Shrivastava S, Moul JW, Xu LL, Segawa T;

WPI; 2003-898255/82.

P-PSDB; ADH2211.

GENBANK; AF224278.

Polynucleotide array, useful for diagnosing or prognosing prostate cancer, comprises a planar, non-porous solid support and a set of polynucleotide probes attached to the solid support.

Disclosure; SEQ ID NO 1; 61bp; English.

The present invention relates to the identification and characterization of a novel androgen-regulated genes (ARGs) that exhibits abundant expression in prostate tissue. The novel gene is designated PMEPA1. The invention is useful for diagnosing and prognosing prostate cancer. The invention is also useful in hormonal therapy. The present sequence is human PMEPA1 cDNA. The PMEPA1 gene is located on chromosome 20q13.

Sequence 1140 BP; 271 A; 349 C; 336 G; 184 T; 0 U; 0 Other;

Query Match 60.6%; Score 800; DB 10; Length 1140;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

522 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGTGTGATGATGTTGGTGG 581

99 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGTGTGATGATGTTGGTGG 158

582 TGATCAGTGTCTGTGAGCCACTACAGCTGTCTGACGCTCTTCATCAGCCGAC 641

159 TGATCAGTGTCTGTGAGCCACTACAGCTGTCTGACGCTCTTCATCAGCCGAC 218

642 GCCAGGGGGAGGAGAGATGATGCTGTCTCAGAGGATGCTGTGGCCCTCGAGA 701

219 GCCAGGGGGAGGAGAGATGATGCTGTCTCAGAGGATGCTGTGGCCCTCGAGA 278

702 GCACAGTGTCTGAGCAACGGAATCCAGAGCCGAGGTCTACGCCGCTCGGCCAC 761

279 GCACAGTGTCTGAGCAACGGAATCCAGAGCCGAGGTCTACGCCGCTCGGCCAC 338

762 ACCGCTGTGGCGGCTTGTGGCCAGCGGAGGCTTCCACGCTTCCAGCCCACT 821

339 ACCGCTGTGGCGGCTTGTGGCCAGCGGAGGCTTCCACGCTTCCAGCCCACT 938

QY	822	ATCCGTACCTGCAGCAGCAGATCGACCTGCACCCACCATCTCGCTGTGACAGCGGAGG	881
Db	399	ATCCGTACCTGCAGCAGCAGATCGACCTGCACCCACCATCTCGCTGTGACAGCGGAGG	458
QY	882	AGCCCCACCTACACAGGGCCCTGCACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGG	941
Db	459	AGCCCCACCTACACAGGGCCCTGCACCTTCAGCTTCGGGACCCCGAGCAGCAGCTGG	518
QY	942	AACTGAACCGGAGTGGTGGCGGCAACCCGCAAGAACCAATCTTTCGACAGTGA	1001
Db	519	AACTGAACCGGAGTGGTGGCGGCAACCCGCAAGAACCAATCTTTCGACAGTGA	578
QY	1002	TGGATAGTGCAGGCTGGCGGCGCCCTGCGGCAACCCGCAAGAACCAATCTTTCGACAGTGA	1061
Db	579	TGGATAGTGCAGGCTGGCGGCGCCCTGCGGCAACCCGCAAGAACCAATCTTTCGACAGTGA	638
QY	1062	CGTGTACCGCAGCGCGGCGGCGCATGAGAGGGCGCGCCCGCCACCTACAGCAGGTCTATCG	1121
Db	639	CGTGTACCGCAGCGCGGCGGCGCATGAGAGGGCGCGCCCGCCACCTACAGCAGGTCTATCG	698
QY	1122	GCCACTACCGGGGTCTCTTCCAGCACCAGAGCAGTGGCGCCCTCTCTTCTGCTGG	1181
Db	699	GCCACTACCGGGGTCTCTTCCAGCACCAGAGCAGTGGCGCCCTCTCTTCTGCTGG	758
QY	1182	AGGGGACCCGGCTCCACACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCA	1241
Db	759	AGGGGACCCGGCTCCACACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCA	818
QY	1242	AAAGAGAGATAAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGCGGCTGGGG	1301
Db	819	AAAGAGAGATAAACAGAAAGACACCTCTCTAGGGTCCCCAGGGGGCGCGGCTGGGG	878
QY	1302	CTGCGTAGTGTAAGAGGCGAG 1321	
Db	879	CTGCGTAGTGTAAGAGGCGAG 898	
RESULT 14			
ID	ADO39826		
XX	ADO39826 standard; cDNA; 1140 BP.		
AC	ADO39826;		
XX			
DT	29-JUL-2004 (first entry)		
XX			
DE	Human PMEPA1 cDNA #1.		
XX			
KW	Androgen-regulated gene; ARG; PMEPA1; prostate cancer; Cap;		
XX	prostate-related disease; gene therapy; vaccine; human; gene; ss.		
OS	Homo sapiens.		
XX			
PH	Key Location/Qualifiers		
FT	95..853		
FT	/tag= a		
FT	/product= "Human PMEPA1 protein"		
XX			
PN	US2004092469-A1.		
XX			
PD	13-MAY-2004.		
XX			
XX	09-MAY-2003; 2003US-00434479.		
XX			
PR	28-JAN-2000; 2000US-0178772P.		
PR	31-JAN-2000; 2000US-0179045P.		
PR	26-JAN-2001; 2001US-00769482.		
PR	18-MAR-2003; 2003US-00390045.		
XX			
PA	(SRIV/) SRIVASTAVA S.		
PA	(MOUL/) MOUL J W.		
PA	(XULL/) XU L L.		
XX			

[illegible]

Search completed: February 19, 2005, 19:26:52
Job time : 712.116 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	800	60.6	1140	4	US-09-769-482-1	Sequence 1, Appli
2	755	57.2	759	4	US-09-769-482-2	Sequence 2, Appli
C 3	34	2.6	640	4	US-09-640-211A-146	Sequence 146, App
C 4	31	2.3	359	4	US-09-640-211A-1198	Sequence 1198, Ap
C 5	31	2.3	533	4	US-09-640-211A-1340	Sequence 1340, Ap
C 6	30	2.3	11729	4	US-09-949-016-13247	Sequence 13247, A
7	30	2.3	142783	4	US-09-949-016-15127	Sequence 15127, A
C 8	29	2.2	3430	4	US-09-949-016-1563	Sequence 1283, Ap
C 9	29	2.2	9406	4	US-09-949-016-13005	Sequence 13005, A
C 10	29	2.2	13832	4	US-09-949-016-17419	Sequence 17419, A
C 11	29	2.2	34230	4	US-09-949-016-12052	Sequence 12052, A
C 12	29	2.2	128470	4	US-09-949-016-13765	Sequence 13765, A
13	28	2.1	700	3	US-09-236-097-7	Sequence 7, Appli
14	28	2.1	1203	3	US-09-086-010-1	Sequence 1, Appli
15	28	2.1	3765	3	US-07-705-490-1	Sequence 1, Appli
16	28	2.1	3765	3	US-07-751-891B-1	Sequence 1, Appli
17	28	2.1	4362	2	US-08-455-073A-1	Sequence 1, Appli
C 18	28	2.1	10348	2	US-08-457-273B-41	Sequence 41, Appl
C 19	28	2.1	10348	3	US-08-556-419-13	Sequence 13, Appl
C 20	28	2.1	10348	3	US-09-041-886-14	Sequence 14, Appl
C 21	28	2.1	10366	1	US-08-246-982A-5	Sequence 5, Appli
C 22	28	2.1	10366	1	US-08-453-265-5	Sequence 5, Appli
23	28	2.1	43117	4	US-09-949-016-17589	Sequence 17589, A
24	27	2.0	402	4	US-09-854-133-418	Sequence 418, App
C 25	27	2.0	8983	4	US-09-949-016-15437	Sequence 15437, A
C 26	27	2.0	154746	4	US-09-827-688-8	Sequence 8, Appli
C 27	27	2.0	154746	4	US-09-827-688-8	Sequence 8, Appli


```
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 78
    |||||
Db 226 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 193

RESULT 4
US-09-640-211A-1198/c
; Sequence 1198, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1198
; LENGTH: 359
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1198

Query Match 2.3%; Score 31; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 75
    |||||
Db 206 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 176

RESULT 5
US-09-640-211A-1340/c
; Sequence 1340, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1340
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1340

Query Match 2.3%; Score 31; DB 4; Length 533;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 75
    |||||
Db 97 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 67

RESULT 6
US-09-949-016-13247
; Sequence 13247, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13247
; LENGTH: 11729
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13247

Query Match 2.3%; Score 30; DB 4; Length 11729;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 74
    |||||
Db 10019 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 10048

RESULT 7
US-09-949-016-15127
; Sequence 15127, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15127
; LENGTH: 142783
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(142783)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15127

Query Match 2.3%; Score 30; DB 4; Length 142783;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 GTGGTGTGATGATGATGATGATGATGATG 583
    |||||
Db 23669 GTGGTGTGATGATGATGATGATGATG 23698

RESULT 8
US-09-949-016-1263/c
; Sequence 1263, Application US/09949016
; Patent No. 6812339
```



```

: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 1263
: LENGTH: 3430
: TYPE: DNA
: ORGANISM: Human
: US-09-949-016-1263

```

```
Query Match      2.2%; Score 29; DB 4; Length 3430;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

RESULT 9
US-09-949-016-13005/c
; Sequence 13005, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13005
; LENGTH: 9406
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13005

```

```

Query Match      2.2%; Score 29; DB 4; Length 9406;
Best Local Similarity 100.0%; Pred. NO. 0.0039;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      557 GTGGTGATGATGGTGATGGTGCGGTGAT 585
Db      2802 GTGGTGATGATGGTGATGGTGCGGTGAT 2774

```

RESULT 10
US-09-949-016-17419/c
; Sequence 17419, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0011307

```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17419
; LENGTH: 13832
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(13832)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17419

```

```

Query Match      2.2%; Score 29; DB 4; Length 13832;
Best Local Similarity 100.0%; Prod. No. 0.0038;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 TGAGGAGGAGGAGCGCGCGCGCGCGCGG 72
      |||||
Db 1875 TGAGGAGGAGGAGCGCGCGCGCGCGCGG 1847

```

RESULT 11
US-09-949-016-12052/c
Sequence 12052, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12052
LENGTH: 34230
TYPE: DNA
ORGANISM: Human
US-09-949-016-12052

```

Query Match      2.2%; Score 29; DB 4; Length 34230;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      555  TGGTGGTGCATGCGTGCATGCGTGCGTG 583
      |||||
Db      4653  TGGTGGTGCATGCGTGCATGCGTGCGTG 4625

```

RESULT 12
US-09-949-016-13765/c
; Sequence 13765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949_016

;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13765
;; LENGTH: 128470
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13765

Query Match 2.2%; Score 29; DB 4; Length 128470;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 555 TGGTGTGATGATGATGATGATGATGATG 583
Db 98598 TGGTGTGATGATGATGATGATGATG 98570

RESULT 13

US-09-236-097-7
; Sequence 7, Application US/09236097
; Patent No. 6335165
; GENERAL INFORMATION:
; APPLICANT: NIR NAVOT ET AL
; TITLE OF INVENTION: METHODS AND KITS FOR CHARACTERIZING GC
; TITLE OF INVENTION: -RICH NUCLEIC ACID SEQUENCES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 20001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,097
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; APPLICANT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 128/33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-09-236-097-7
Query Match 2.1%; Score 28; DB 3; Length 700;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 83
Db 505 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 532

RESULT 14

US-09-086-010-1
; Sequence 1, Application US/09086010
; Patent No. 6274338
; GENERAL INFORMATION:
; APPLICANT: Glimcher, Laurie H. et al.
; TITLE OF INVENTION: Human c-Maf Compositions and
; TITLE OF INVENTION: Methods of Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,010
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/030,579
; APPLICATION NUMBER:
; FILING DATE: 2-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: HUI-027CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1203 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1203
US-09-086-010-1

Query Match 2.1%; Score 28; DB 3; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 83
Db 679 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 706

RESULT 15

US-07-705-490-1
; Sequence 1, Application US/07705490
; Patent No. 6107025
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
; APPLICANT: Nelson, David L.
; APPLICANT: Pieretti, Maura
; APPLICANT: Warren, Stephen T.
; APPLICANT: Oostria, Ben A.
; TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome

/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Thomas D. Paul
/ STREET: 1301 McKinney, Suite 5100
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.A.
/ ZIP: 77010-3095
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/705,490
/ FILING DATE: 19910708
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul, Thomas D.
/ REGISTRATION NUMBER: 32,714
/ REFERENCE/DOCKET NUMBER: D-5350
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/651-5325
/ TELEFAX: 713/651-5246
/ TELEX: 762829
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3765 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-07-705-490-1

Query Match 2.1%; Score 28; DB 3; Length 3765;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 83
|||||
Db 44 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 71

Search completed: February 20, 2005, 00:05:25
Job time : 246.979 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 19:27:04 ; Search time 742.23 Seconds
(without alignments)
10519.334 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgggtctcgagcgca.....ctgcgtaggtgaaagcgag 1321

Scoring table:

OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 5384158 seqs, 2955248155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	9	US-09-934-249-1
2	1229	93.0	4839	15	US-10-241-220-119
3	1229	93.0	4839	16	US-10-269-909-84
4	1229	93.0	4839	16	US-10-269-909-85
5	1229	93.0	4839	18	US-10-872-972-119
6	1229	93.0	4839	18	US-10-872-991-119
7	864	65.4	864	17	US-10-295-027-127
8	861	65.2	861	9	US-09-934-249-3
9	800	60.6	1140	16	US-10-390-045-1
10	800	60.6	1140	17	US-10-434-479-1
11	800	60.6	1141	15	US-10-205-823-412

12	800	60.6	1141	15	US-10-301-822-208	Sequence 208, App	
13	800	60.6	1850	15	US-10-241-220-44	Sequence 44, Appl	
14	800	60.6	1850	18	US-10-872-972-44	Sequence 44, Appl	
15	800	60.6	1850	18	US-10-872-991-44	Sequence 44, Appl	
16	800	60.6	4527	10	US-09-821-812-2	Sequence 2, Appl1	
17	800	60.6	4527	18	US-10-849-635-2	Sequence 2, Appl1	
18	788	59.7	1066	13	US-10-098-841-71	Sequence 71, Appl1	
19	755	57.2	759	16	US-10-390-045-2	Sequence 2, Appl1	
20	755	57.2	759	17	US-10-434-479-2	Sequence 2, Appl1	
21	749	56.7	969	10	US-09-796-753-55	Sequence 55, Appl	
22	713	54.0	806	15	US-10-241-220-45	Sequence 45, Appl	
23	713	54.0	806	18	US-10-872-972-45	Sequence 45, Appl	
24	713	54.0	806	18	US-10-872-991-45	Sequence 45, Appl	
25	560	42.4	1583	14	US-10-000-256A-32	Sequence 32, Appl	
c	26	302	22.9	693	9	US-09-934-249-14	Sequence 14, Appl
27	178	13.5	467	10	US-09-918-995-2074	Sequence 2074, Ap	
28	102	7.7	368	9	US-09-783-590-3464	Sequence 3464, Ap	
29	60	4.5	60	10	US-09-908-975-13620	Sequence 13620, A	
30	56	4.2	522	17	US-10-240-425-166	Sequence 166, App	
31	50	3.8	65	9	US-09-783-590-3488	Sequence 3488, Ap	
32	45	3.4	837	18	US-10-363-345A-30091	Sequence 30091, A	
c	33	45	3.4	837	18	US-10-363-345A-30092	Sequence 30092, A
34	44	3.3	878	9	US-09-934-249-12	Sequence 12, Appl	
35	44	3.3	1713	10	US-09-796-753-57	Sequence 57, Appl	
36	41	3.1	475	9	US-09-934-249-15	Sequence 15, Appl	
c	37	37	2.8	837	18	US-10-363-345A-30089	Sequence 30089, A
38	37	2.8	837	18	US-10-363-345A-30090	Sequence 30090, A	
39	34	2.6	555	18	US-10-425-115-66221	Sequence 66221, A	
c	40	34	2.6	640	18	US-10-856-499-146	Sequence 146, App
c	41	34	2.6	1050	18	US-10-739-930-3690	Sequence 3690, Ap
c	42	34	2.6	1752	18	US-10-437-963-48088	Sequence 48088, A
c	43	34	2.6	2000	17	US-10-260-238-2427	Sequence 2427, Ap
44	32	2.4	577	9	US-09-864-761-20542	Sequence 20542, A	
45	32	2.4	630	18	US-10-437-963-45057	Sequence 45057, A	

ALIGNMENTS

RESULT 1

- US-09-934-249-1
- Sequence 1, Application US/09934249
- Patent No. US20020115081A1
- GENERAL INFORMATION:
- APPLICANT: Lee, Richard T.
- APPLICANT: Landschulz, Katherine T.
- APPLICANT: Turi, Thomas G.
- APPLICANT: Thompson, John P.
- APPLICANT: Kennedy, Scott P.
- TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
- TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
- FILE REFERENCE: P0738/7001/ERP/KA
- CURRENT APPLICATION NUMBER: US/09/934, 249
- CURRENT FILING DATE: 2001-08-21
- PRIOR APPLICATION NUMBER: US 60/227,159
- PRIOR FILING DATE: 2000-08-22
- NUMBER OF SEQ ID NOS: 17
- SOFTWARE: FastSeq for Windows Version 3.0
- SEQ ID NO 1
- LENGTH: 1321
- TYPE: DNA
- ORGANISM: Homo Sapiens
- FEATURE:
- NAME/KEY: CDS
- LOCATION: (413)...(1273)

Query Match 100.0%; Score 1321; DB 9; Length 1321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGGCTCTCGAGCGCAACCCGATCTCTTGACTTGAATGAGGAGGCGCG 60
|||||

Db 1 CGACCGCGGTCTCGAGCGGAAACCCGATCTCTTGGACTTGAATAGAGAGAGAGCGCG 60
Qy 61 CGGCGCGGCGCGCGAGCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120
Db 61 CGGCGCGGCGCGCGAGCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120
Qy 121 GCGGAGAGCGCGCGCGCTCGGCTCGGAGCGCAATTTTCGGAGCGCAACCGCGGGGACTGCGG 180
Db 121 GCGGAGAGCGCGCGCGCTCGGCTCGGAGCGCAATTTTCGGAGCGCAACCGCGGGGACTGCGG 180
Qy 181 ACSCCCCCGGGCTGCGAGGAGGAGCGCGGGGGGCGCAGGAGCGCGTCCCGCGCAC 240
Db 181 ACSCCCCCGGGCTGCGAGGAGGAGCGCGGGGGGCGCAGGAGCGCGTCCCGCGCAC 240
Qy 241 TGAGCCCCCGGCGCGCGCGGAACTTGGCGGCGCAACCGAGCCCGGCGAGCGCGGGCGCG 300
Db 241 TGAGCCCCCGGCGCGCGCGGAACTTGGCGGCGCAACCGAGCCCGGCGAGCGCGGGCGCG 300
Qy 301 CTCCTCCCGCGCGCGCTCTCTGATGCGGGGCCCTCAGCTCCGGGCGCGCGCGAGCCCC 360
Db 301 CTCCTCCCGCGCGCGCTCTCTGATGCGGGGCCCTCAGCTCCGGGCGCGCGCGAGCCCC 360
Qy 361 CCCG 420
Db 361 CCCG 420
Qy 421 CTTGATGGGGGTCAACAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 421 CTTGATGGGGGTCAACAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 481 GTGCACTGCAACCGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTGTCA 540
Db 481 GTGCACTGCAACCGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTGTCA 540
Qy 541 GATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 541 GATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Qy 601 CCACTACAAGCTCTGTCAGCGTCTTTCATCAGCGCGCAAGCGCGGCGAGGAGAGA 660
Db 601 CCACTACAAGCTCTGTCAGCGTCTTTCATCAGCGCGCAAGCGCGGCGAGGAGAGA 660
Qy 661 AGATGCTCTCTCAGAGATGCTGTGGCTCTGGAGGACACAGTGTACGGCAACGG 720
Db 661 AGATGCTCTCTCAGAGATGCTGTGGCTCTGGAGGACACAGTGTACGGCAACGG 720
Qy 721 AATCCAGAGCGCGAGTGTACCGCGCTCTGGCGCCACCGCGCGCTGCGCGTGGCGC 780
Db 721 AATCCAGAGCGCGAGTGTACCGCGCTCTGGCGCCACCGCGCGCTGCGCGTGGCGC 780
Qy 781 CTTTCGCGCGAGCGGCTTTCACCGCTTTCAGCGCCACCTATCTCGTACCTGACACGA 840
Db 781 CTTTCGCGCGAGCGGCTTTCACCGCTTTCAGCGCCACCTATCTCGTACCTGACACGA 840
Qy 841 GATGCACTGCAACCACTCTCGTGTGACGCGGAGGAGCCCGCCACCTTACAGGG 900
Db 841 GATGCACTGCAACCACTCTCGTGTGACGCGGAGGAGCCCGCCACCTTACAGGG 900
Qy 901 CCCCTGCACTCCAGCTTCGGAGCCCGGAGCAGCAGTGGAACTGAAACCGGAGTCGT 960
Db 901 CCCCTGCACTCCAGCTTCGGAGCCCGGAGCAGCAGTGGAACTGAAACCGGAGTCGT 960
Qy 961 GCGCGCAACCCCAACAGAACCACTTCGACAGTGAACCTGATGATGATGATGATGATGATG 1020
Db 961 GCGCGCAACCCCAACAGAACCACTTCGACAGTGAACCTGATGATGATGATGATGATGATG 1020
Qy 1021 CGGCCCTGCCCCCAGCAGTAACTCGGCACTCAGCGCACGTGCTTACGGCAGCGCGG 1080
Db 1021 CGGCCCTGCCCCCAGCAGTAACTCGGCACTCAGCGCACGTGCTTACGGCAGCGCGG 1080
Qy 1081 GCGCATGGAGGGCGCGCGCCCACTACAGGAGTTCATCGGCCACTACCGGGGTCTTC 1140
Db 1081 GCGCATGGAGGGCGCGCGCCCACTACAGGAGTTCATCGGCCACTACCGGGGTCTTC 1140

RESULT 2

US-10-241-220-119
; Sequence 119, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-119

Query Match 93.0%; Score 1229; DB 15; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAAGCTAGCGGAGAGCTCAGCCCGCGGCGAGCGCGCGCTGCGAGGCCCATTT 152
Db 1 GGAAAGCTAGCGGAGAGCTCAGCCCGCGGCGAGCGCGCGCTGCGAGGCCCATTT 60
Qy 153 TTCGGAGCGCAACCGCGGCGACTGCGGACCGCCCGGGGCTGCCAGGGAGCGCGGG 212
Db 61 TTCGGAGCGCAACCGCGGCGACTGCGGACCGCCCGGGGCTGCCAGGGAGCGCGGG 120
Qy 213 GCGCGCAGCGGAGCGCGTCCCGCGCACTGAGCCCGCGGCGCCCGGAGAACTTGGCGGC 272
Db 121 GCGCGCAGCGGAGCGCGTCCCGCGCACTGAGCCCGCGGCGCCCGGAGAACTTGGCGGC 180
Qy 273 GACCCGAGCGCGGAGCGCGCGCTTCCCGCGCGCGCGCTTCTGCAATGCGGGGC 332
Db 181 GACCCGAGCGCGGAGCGCGCGCTTCCCGCGCGCGCGCTTCTGCAATGCGGGGC 240
Qy 333 CCCAGCTCCGGGCGCGCGCGGAGCCCGCCCGCGCGCGCCCGGAGCCCGCGCGCGCG 392
Db 241 CCCAGCTCCGGGCGCGCGCGGAGCCCGCCCGCGCGCGCCCGGAGCCCGCGCGCGCG 300
Qy 393 GCGCGCGCGCGCGCGCGCTTCCATGCACTGAGGGGTCAACAGACACCGCGCGCGCG 452
Db 301 GCGCGCGCGCGCGCGCTTCCATGCACTGAGGGGTCAACAGACACCGCGCGCGCG 360
Qy 453 CCGCGGCGAGCGCCCAATGCTCTCTGCACTGCAAACTGTTTGTTCAGAGCA 512
Db 453 CCGCGGCGAGCGCCCAATGCTCTCTGCACTGCAAACTGTTTGTTCAGAGCA 512


```
QY 593 CTGCTGAGCCACTACAGCTGTCTGACAGCTCTTCTCATCAGCGGCACAGCCAGCGGCGG 652
Db 181 CTGCTGAGCCACTACAGCTGTCTGACAGCTCTTCTCATCAGCGGCACAGCCAGCGGCGG 240
QY 653 AGGAGAGAAGATGCCCTGTCTCTCAGAAAGGATGCTGTGGCCCTCGAGAGACACAGTGTCA 712
Db 241 AGGAGAGAAGATGCCCTGTCTCTCAGAAAGGATGCTGTGGCCCTCGAGAGACACAGTGTCA 300
QY 713 GGCACAGGAATCCAGAGCCGCGAGGTCTACGCCGCCCGCTCGGSCCACCAGACGCGCTGGCC 772
Db 301 GGCACAGGAATCCAGAGCCGCGAGGTCTACGCCGCCCGCTCGGSCCACCAGACGCGCTGGCC 360
QY 773 GTGCGGCCCTTCGCCAGCGGCGGCGCTTCCACGCTTCAGGCCCACTATCGGTACCTG 832
Db 361 GTGCGGCCCTTCGCCAGCGGCGGCGCTTCCACGCTTCAGGCCCACTATCGGTACCTG 420
QY 833 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTGACAGCGGAGGAGCCGCCACCC 892
Db 421 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTGACAGCGGAGGAGCCGCCACCC 480
QY 893 TACAGGGGCCCTTGCACTTCCAGCTTCGGGAGCCCGAGCAGCAGCTTGGAACTGAAACCGG 952
Db 481 TACAGGGGCCCTTGCACTTCCAGCTTCGGGAGCCCGAGCAGCAGCTTGGAACTGAAACCGG 540
QY 953 GAGTCGCTGCGCGCACCCCAACAGAACCATCTTTCGACAGTGCATCTGATGGATAGTGC 1012
Db 541 GAGTCGCTGCGCGCACCCCAACAGAACCATCTTTCGACAGTGCATCTGATGGATAGTGC 600
QY 1013 AGCTGCGGCGCCCTTGCGCCCCCAGCAGTAACCTCGGGCATCAGCGCCAGCTGCTACGGC 1072
Db 601 AGCTGCGGCGCCCTTGCGGGCGCGCGCGCCACCTACAGCGAGGTCTATCGGSCACTACCGG 720
QY 1133 GGGTCTCTCTTCAGCAGCAGCAGAGAGAGTGGGCGCGCCCTCTTCTGAGGGGAGCCCGG 1192
Db 721 GGGTCTCTCTTCAGCAGCAGCAGAGAGAGTGGGCGCGCCCTCTTCTGAGGGGAGCCCGG 780
QY 1193 CTCACACACACACATCGCGGCCCTTAGAGAGCGAGCAGCATCTGGAGCAAGAGAGGAT 1252
Db 781 CTCACACACACACATCGCGGCCCTTAGAGAGCGAGCAGCATCTGGAGCAAGAGAGGAT 840
```

RESULT 8

```
US-09-934-249-3
; Sequence 3, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John P.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934,249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
```

```
; NAME/KEY: CDS
; LOCATION: (1)... (861)
US-09-934-249-3
```

```
Query Match 65.2%; Score 861; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 413 ATGCACCGCTTGTATGGGGGTCAAACAGCACCGCCGCGCGCCGCGCGGCGAGCCCAATGTC 472
Db 1 ATGCACCGCTTGTATGGGGGTCAAACAGCACCGCCGCGCGCCGCGCGGCGAGCCCAATGTC 60
QY 473 TCCTGCACGTCGCAACTGCAAAACGCTCTTGTTCAGAGCATGAGATCAGGAGCTGGAG 532
Db 61 TCCTGCACGTCGCAACTGCAAAACGCTCTTGTTCAGAGCATGAGATCAGGAGCTGGAG 120
QY 533 TTTGTTTCAGATCATCATCGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 592
Db 121 TTTGTTTCAGATCATCATCGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 593 CTGCTGAGCCACTCAAGCTGTCTGCAAGCTCTTTCATCAGCGGCGCACAGCCAGGGCGG 652
Db 181 CTGCTGAGCCACTCAAGCTGTCTGCAAGCTCTTTCATCAGCGGCGCACAGCCAGGGCGG 240
QY 653 AGGAGAGAAGATGCCCTGTCTCTCAGAAAGGATGCTGTGGCCCTCGAGAGACACAGTGTCA 712
Db 241 AGGAGAGAAGATGCCCTGTCTCTCAGAAAGGATGCTGTGGCCCTCGAGAGACACAGTGTCA 300
QY 713 GGCACAGGAATCCAGAGCCGCGAGGTCTACGCCCGCGCTCGGCCACCGACCGCTGGCC 772
Db 301 GGCACAGGAATCCAGAGCCGCGAGGTCTACGCCCGCGCTCGGCCACCGACCGCTGGCC 360
QY 773 GTGCGGCCCTTCGCCCCAGCGGGAGCGCTTCCACGCTTCAGGCCCACTTATCGGTACCTG 832
Db 361 GTGCGGCCCTTCGCCCCAGCGGGAGCGCTTCCACGCTTCAGGCCCACTTATCGGTACCTG 420
QY 833 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTGACAGCGGAGGAGCCGCCACCC 892
Db 421 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTGACAGCGGAGGAGCCGCCACCC 480
QY 893 TACAGGGGCCCTTGCACTTCCAGCTTCGGGAGCCCGAGCAGCAGCTTGGAACTGAAACCGG 952
Db 481 TACAGGGGCCCTTGCACTTCCAGCTTCGGGAGCCCGAGCAGCAGCTTGGAACTGAAACCGG 540
QY 953 GAGTCGCTGCGCGCACCCCAACAGAACCATCTTTCGACAGTGCATCTGATGGATAGTGC 1012
Db 541 GAGTCGCTGCGCGCACCCCAACAGAACCATCTTTCGACAGTGCATCTGATGGATAGTGC 600
QY 1013 AGGTCGGGCGGCCCTTCGCCCGCCAGAGTAACCTCGGGCATCAGCGCCAGCTGCTACGGC 1072
Db 601 AGGTCGGGCGGCCCTTCGCCCGCCAGAGTAACCTCGGGCATCAGCGCCAGCTGCTACGGC 660
QY 1073 AGCGGGGCGCATGGAGGGGCGCGCCACCTACAGCGAGGTCTATCGGSCACTACCGG 1132
Db 661 AGCGGGGCGCATGGAGGGGCGCGCCACCTACAGCGAGGTCTATCGGSCACTACCGG 720
QY 1133 GGGTCTCTCTTCAGCAGCAGCAGAGAGTGGGCGCGCCCTCTTCTGAGGGGAGCCCGG 1192
Db 721 GGGTCTCTCTTCAGCAGCAGCAGAGAGTGGGCGCGCCCTCTTCTGAGGGGAGCCCGG 780
QY 1193 CTCACACACACACATCGCGGCCCTTAGAGAGCGAGCAGCATCTGGAGCAAGAGAGGAT 1252
Db 781 CTCACACACACACATCGCGGCCCTTAGAGAGCGAGCAGCATCTGGAGCAAGAGAGGAT 840
QY 1253 AAACAGAAAGGACACCCCTCTC 1273
Db 841 AAACAGAAAGGACACCCCTCTC 861
```

RESULT 9

```
US-10-390-045-1
; Sequence 1, Application US/10390045
; Publication No. US20030170713A1
```


Query Match	60.6%; Score 800; DB 15; Length 1141;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	522 CGGAGCTCGAGTGTGTTTCAGATCATCATCATGTGTGTGTGATGATGGTGATGGTGCG 581
Db	100 CGGAGCTCGAGTGTGTTTCAGATCATCATCATGTGTGTGTGATGATGGTGATGGTGCG 159
QY	582 TGATCACGTGCTGCTGAGGCCATCAAGCTGTCTCAAGCTCTTTCATCAGCGGCACA 641
Db	160 TGATCACGTGCTGCTGAGGCCATCAAGCTGTCTCAAGCTCTTTCATCAGCGGCACA 219
QY	642 GCCAGGGCGGAGAGAGATGSCCTGTCTCACAAGGATGCTGTGGCCCTCGGAGA 701
Db	220 GCCAGGGCGGAGAGAGATGSCCTGTCTCACAAGGATGCTGTGGCCCTCGGAGA 279
QY	702 GCACAGTGTCAAGCAACGGGAATCCAGAGCGCAGGTCTACGCCCGGCTCGGCCACCG 761
Db	280 GCACAGTGTCAAGCAACGGGAATCCAGAGCGCAGGTCTACGCCCGGCTCGGCCACCG 339
QY	762 ACCGCTTGGCCGTCGCGCCCTTCGCCACGCGGAGCGCTTCAACGCTTCACGCCACCT 821
Db	340 ACCGCTTGGCCGTCGCGCCCTTCGCCACGCGGAGCGCTTCAACGCTTCACGCCACCT 399
QY	822 ATCCGTACTCTGACGACGAGATCGACCTTGCACCCACCATCTCGCTGTTCAGACGGGAGG 881
Db	400 ATCCGTACTCTGACGACGAGATCGACCTTGCACCCACCATCTCGCTGTTCAGACGGGAGG 459
QY	882 AGCCCCACCTTACCAGGCGCCCTGCACCTTCAGTTTCGGAGCCCGAGCAGCAGCTGG 941
Db	460 AGCCCCACCTTACCAGGCGCCCTGCACCTTCAGTTTCGGAGCCCGAGCAGCAGCTGG 519
QY	942 AACTGAACCGGGAGTCGGTTCGGCGCACCCGCCCAACAGAACATCTTTCAGACAGTCACCTGA 1001
Db	520 AACTGAACCGGGAGTCGGTTCGGCGCACCCGCCCAACAGAACATCTTTCAGACAGTCACCTGA 579
QY	1002 TGGATAGTGCACGCTTGGGCGGCCCTTGCCGCCCCAGCAGATACTTCGGGCATCAGCGCCA 1061
Db	580 TGGATAGTGCACGCTTGGGCGGCCCTTGCCGCCCCAGCAGATACTTCGGGCATCAGCGCCA 639
QY	1062 CGTGCTACGGCAGCGGCGGCGCATGAGGGGCGCGCCGCCACCTTACAGCGAGGTCTATCG 1121
Db	640 CGTGCTACGGCAGCGGCGGCGCATGAGGGGCGCGCGCCGCCACCTTACAGCGAGGTCTATCG 699
QY	1122 GCCACTACCGGGGTCTCTTCTCCAGCACACGACAGCAGTGGGCGGCCCTCTCTGCTGG 1181
Db	700 GCCACTACCGGGGTCTCTTCTCCAGCACACGACAGCAGTGGGCGGCCCTCTCTGCTGG 759

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 18:35:57 ; Search time 4154.91 Seconds
(without alignments)
12102.031 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcgagcgca.....ctgcgtaggtgaaagggcag 1321

Scoring table:
OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	741	56.1	901	3	CR612083 full-leng
2	632	47.8	1046	5	BM922276 AGENCOURT
3	614	46.5	967	5	BQ641849 AGENCOURT
4	568	43.0	916	5	BQ954555 AGENCOURT
5	558	42.2	609	5	BQ636742 hdl3h06.y
6	550	41.6	551	4	BM141979 if25all.y
7	536	40.6	605	7	CV028567 7115 Full
8	533	40.3	850	1	AL558881 AL558881
9	518	39.2	729	5	BQ575741 UI-H-EZ1-
10	511	38.7	850	5	BU602918 AGENCOURT
11	497	37.6	890	5	BQ690750 AGENCOURT
12	474	35.9	572	5	BX641317 DKFZp686K
13	471	35.7	1068	5	BQ527705 AGENCOURT
14	468	35.4	655	5	BQ691705 AGENCOURT
15	450	34.1	964	5	BU859860 AGENCOURT
16	449	34.0	945	5	BU539219 AGENCOURT
17	445	33.7	782	5	BQ015170 AGENCOURT
18	442	33.5	602	6	CA431191 UI-H-FG1-
19	442	33.5	780	9	AY419334 Homo sapi
20	441	33.4	461	4	BM712680 UI-E-EJ0-
21	437	33.1	633	4	BM714472 UI-E-EJ0-
22	428	32.4	588	5	BU624784 UI-H-FG1-
23	425	32.2	897	1	AL558882 AL558882
24	424	32.1	1038	1	AL517150 AL517150

25	422	31.9	844	5	BQ686793	BQ686793 AGENCOURT
26	422	31.9	938	5	BU157842	BU157842 AGENCOURT
27	422	31.9	952	5	BU157959	BU157959 AGENCOURT
28	422	31.9	1280	5	BQ691500	BQ691500 AGENCOURT
C	29	417	31.6	559	2	BE855409 7g13f05.x
C	30	417	31.6	629	5	BU730650 UI-E-C11-
C	31	406	30.7	1400	4	BM559329 AGENCOURT
C	32	401	30.4	730	4	BM677602 UI-E-B01-
C	33	399	30.2	626	5	BM974296 UI-CF-EC1
C	34	395	29.9	544	7	CN296134 170006001
C	35	393	29.8	728	5	BU683523 UI-CF-EC1
C	36	390	29.5	973	5	BU169156 AGENCOURT
C	37	383	29.0	570	5	BQ575582 UI-H-EZ1-
C	38	377	28.5	563	6	CB049800 NISC_gj13
39	365	27.6	552	4	BM713900	BM713900 UI-E-EJ0-
40	358	27.1	1127	5	BU174654	BU174654 AGENCOURT
41	348	26.3	646	5	BU859841	BU859841 AGENCOURT
C	42	338	25.6	867	5	BX362396 BX362396
C	43	331	25.1	899	5	BU196912 AGENCOURT
C	44	327	24.8	547	4	BM676516 UI-E-EJ0-
45	324	24.5	613	4	BG680325	BG680325 602629217

ALIGNMENTS

RESULT 1
LOCUS CR612083 901 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DJ015YF12 of T cells (Jurkat cell line)
Cot 10-normalized of Homo sapiens (human).
ACCESSION CR612083.1 GI:50492890
VERSION HTC; CDSLT CDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 901)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang, Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 901)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Genoscope.
COMMENT Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source 1..901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ015YF12"
/tissue type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 56.1%; Score 741; DB 3; Length 901;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 741; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 581 GTGATCAGTGGCTGCTGAGCCACTACAGCTCTCTGACGGTCTTCATCAGCGGCAC 640
|||||


```
QY 1007 AGTGCAGGCTGGCGGCGCCCTGCCCCCAGCAGTAACCTCGGGCATCAGCGCCACGTGC 1066
|||||
Db 661 AGTGCAGGCTGGCGGCGGCGCCCTGCCCCCAGCAGTAACCTCGGGCATCAGCGCCACGTGC 720
|||||
QY 1067 TACGCGAGCGCGCG 1080
|||||
Db 721 TACGCGAGCGCGCG 734
|||||

RESULT 3
BQ641849
LOCUS
DEFINITION BQ641849 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
5', mRNA sequence.
ACCESSION BQ641849
VERSION BQ641849.1 GI:21766021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2493 row: 9 column: 18
High quality sequence stop: 571.
Location/Qualifiers
1. 967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6292265"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 43"
/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming, Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

ORIGIN
Query Match 46.5%; Score 614; DB 5; Length 967;
Best Local Similarity 99.7%; Pred. No. 2.6e-291;
Matches 714; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 GAGCTGGAGTTTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATGATGATG 593
|||||
Db 1 GAGCTGGAGTTTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATGATGATG 60
|||||

QY 584 ATCAGCTGCTGTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCGGCACAGC 643
|||||
Db 61 ATCAGCTGCTGTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCGGCACAGC 120
|||||

QY 644 CAGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAGGATGCTGTGGCCCTCGGAGAGC 703
|||||
Db 121 CAGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAGGATGCTGTGGCCCTCGGAGAGC 180
|||||

QY 704 ACAGTGTACGGCAACGGAATCCAGAGCCGACGCTACGCCCGCTCGGCCACCGAC 763
|||||
```

```
Db 181 ACAGTGTACGGCAACGGAATCCAGAGCCGACGGTCTACGCCCGCTCGGCCACCGAC 240
QY 764 CGCTTGGCGGTGCGCGCCCTTTCGCCCGCAGCGGAGCGCTTCCACCGCTTCAGGCCACCTAT 823
Db 241 CGCTTGGCGGTGCGCGCCCTTTCGCCCGCAGCGGAGCGCTTCCACCGCTTCAGGCCACCTAT 300
QY 824 CGGTACCTGCAGCAGCAGATCGACCTGCGCACCCACCATCTCGCTGTTCAGACGGGAGGAG 883
Db 301 CGGTACCTGCAGCAGCAGATCGACCTGCGCACCCACCATCTCGCTGTTCAGACGGGAGGAG 360
QY 884 CCCCCACCTTACAGGGCGCCCTTCACCTTCAGCTTCGGGACCCCGCAGCAGCAGCTGGAA 943
Db 361 CCCCCACCTTACAGGGCGCCCTTCACCTTCAGCTTCGGGACCCCGCAGCAGCAGCTGGAA 420
QY 944 CTGAACCGGGAGTGGTGGCGGACCCCCCAAAACAGAACCATCTTCACAGTGAACCTGATG 1003
Db 421 CTGAACCGGGAGTGGTGGCGGACCCCCCAAAACAGAACCATCTTCACAGTGAACCTGATG 480
QY 1004 GATAGTGCAGGCTGGGCGGCGCCCTTCGCCCGCAGCAGTAACCTCGGGCATCAGCGCCACG 1063
Db 481 GATAGTGCAGGCTGGGCGGCGCCCTTCGCCCGCAGCAGTAACCTCGGGCATCAGCGCCACG 540
QY 1064 TGCTACGGCAGCGCGGCGGCATGAGGCGGCGCGCCCGCCACCTTACAGCAGGTCATCGGC 1123
Db 541 TGCTACGGCAGCGCGGCGGCATGAGGCGGCGCGCCCGCCACCTTACAGCAGGTCATCGGC 600
QY 1124 CACTACCGGGGTCTCTCTTCAGACACAGCAGAGAGAGTGGCGCGCTCTCTTCTGGAG 1183
Db 601 CACTACCGGGGTCTCTCTTCAGACACAGCAGAGAGAGTGGCGCGCTCTCTTCTGGAG 660
QY 1184 GGGACCGGCTCCACCACACACATCGCGCGCCCTAGAGAGCGCAGCCATCTCGAG 1239
Db 661 GGGACCGGCTCCACCACACACATCGCGCGCCCTAGAGAGCGCAGCCATCTCGAG 716

RESULT 4
BQ954555
LOCUS
DEFINITION BQ954555 916 bp mRNA linear EST 21-AUG-2002
IMAGE:6204609 5', mRNA sequence.
ACCESSION BQ954555
VERSION BQ954555.1 GI:22370033
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC13626 row: c column: 10
High quality sequence stop: 669.
Location/Qualifiers
1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204609"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic_nerve"
```


QY 931 GCAGCAGTGAAGTGAACCGGAGTGGTGGCGGACCCGACCCCAACAGACCACTCTTCGA 990
Db 301 GCAGCAGTGAAGTGAACCGGAGTGGTGGCGGACCCGACCCCAACAGACCACTCTTCGA 360
QY 991 CAGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCGCCGCCAGCACTAACTCGGG 1050
Db 361 CAGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCGCCGCCAGCACTAACTCGGG 420
QY 1051 CATCAGGCCACGTGCTACGGCAGCGGGGGCGATGAGAGGGGGCGCGGCCACCTACAG 1110
Db 421 CATCAGGCCACGTGCTACGGCAGCGGGGGCGATGAGAGGGGGCGCGGCCACCTACAG 480
QY 1111 CGAGGTGATGGCCACTACCGGGGCTCTCTTCCAGCACCGACAGAGCAGTGGGGCGCC 1170
Db 481 CGAGGTGATGGCCACTACCGGGGCTCTCTTCCAGCACCGACAGAGCAGTGGGGCGCC 540
QY 1171 CTCCTTCTGAGGGGACCGGCTTCCACACACACACATCGCGGCCCTAGAGAGCGCAGC 1230
Db 541 CTCCTTCTGAGGGGACCGGCTTCCACACACACACATCGCGGCCCTAGAGAGCGCAGC 600
QY 1231 CATCTGGAG 1239
Db 601 CATCTGGAG 609

RESULT 6

BM141979

LOCUS

DEFINITION BM141979.1 551 bp mRNA linear EST 12-MAR-2002
if25all.v1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5677341 5' similar to TR:Q9UUD3 Q9UUD3 DUT18J7.1
// mRNA sequence.

ACCESSION

BM141979

VERSION

BM141979.1 GI:17152046

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Seearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wyllie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE

Endocrine Pancreas Consortium

JOURNAL

Unpublished (2000)

COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohpc.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 429.

FEATURES

source

1..551
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5677341"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

CV028567 605 bp mRNA linear EST 20-AUG-2004
7115 Full length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC015918, mRNA sequence.
CV028567
CV028567.1 GI:51486652
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

REFERENCE
AUTHORS
  Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
  Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
  Clingingsmith,T.R., Hartley,J.L., Eposito,D., Cheo,D., Moore,T.,
  Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
  Vandenhaute,J., Cusick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M.
  Human ORFome Version 1.1: a Platform for Reverse Proteomics
  Genome Res. (2004) In press
  Contact: Vidal M
  Marc Vidal Laboratory
  Dana Farber Cancer Institute
  1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
  Tel: 617 632 5180
  Fax: 617 632 5739
  Email: Marc.Vidal@dfci.harvard.edu
  ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
  results from a PCR reaction using an MGC full-length cDNA as
  template DNA and ORF specific primers
  PCR Primers
  FORWARD: ATGATGGTATGGTGGTG
  BACKWARD: TAGAGGGGTCTCTTTCTGT
  Insert Length: 605 Std Error: 45.00
  Plate: 11020 row: 10 Column: D
  Seq primer: ACTGGCGTGTCTTACACGTCTGACTGGGAAAC
  High quality sequence start: 11
  High quality sequence stop: 604
  POLYA=No.

FEATURES
  source
    1..605
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /tissue_type="mixed"
    /clone_lib="Full Length cDNA from the Mammalian Gene
    Collection"
    /notes="vector: mixed; The ORFs were PCR amplified from the
    MGC (Mammalian Gene Collection) as of April 2004 and
    cloned by recombinational Gateway cloning into pDONR223
    Donor vector. Reference : MGC (Mammalian Gene Collection)
    Program Team, Generation and Initial Analysis of more than
    15,000 Full-Length Human and Mouse cDNA Sequences. FNAS,
    2002, 99(26), 16899-16903"

ORIGIN
  Query Match 40.6%; Score 536; DB 7; Length 605;
  Best Local Similarity 99.8%; Pred. No. 8.1e-253;
  Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 577 GGTGGTGTATCAGTGTCTGTGAGCCACTACAAAGCTGTGTGACGGTCTTTCATCAGCGG 636
DB 15 GGTGGTGTATCAGTGTCTGTGAGCCACTACAAAGCTGTGTGACGGTCTTTCATCAGCGG 74
QY 637 GCACAGCCAGGGCGGAGGAGAGAGATGCCCTGTCTCTCAGAGGATGCTGTGGCCCTC 696
DB 75 GCACAGCCAGGGCGGAGGAGAGAGATGCCCTGTCTCTCAGAGGATGCTGTGGCCCTC 134
QY 697 GGAGAGACAGTGTCTGAGCAACCGAATCCAGAGCCGCGAGGTCTAGCCCGCGCTCGGCC 756
DB 135 GGAGAGACAGTGTCTGAGCAACCGAATCCAGAGCCGCGAGGTCTAGCCCGCGCTCGGCC 194
QY 757 CACCGACCGCTGGCGGTGGCGCCCTTCGCCAGCGGAGCGGCTTCACCGCTTCAGCC 816
DB 195 CACCGACCGCTGGCGGTGGCGCCCTTCGCCAGCGGAGCGGCTTCACCGCTTCAGCC 254
QY 817 CACTATCCGTACTCTCAGCAGCAGAGATCGACCTGCGCCACCCACCATCTGCTGTCTCAGCGG 876
DB 255 CACTATCCGTACTCTCAGCAGCAGAGATCGACCTGCGCCACCCACCATCTGCTGTCTCAGCGG 314
QY 877 GGAGAGCCCCCACCCTTACAGGGCCCCCTGACCCCTTCCAGCTTTCGGGACCCCGAGCAGCA 936
DB 315 GGAGAGCCCCCACCCTTACAGGGCCCCCTGACCCCTTCCAGCTTTCGGGACCCCGAGCAGCA 374
QY 937 GCTTGAAGTAAGTGAACGGGAGTCTGGTGGCGGACCCCGGAGAGATGCTGTGGCCCTTCGAGAGCA 996

```

```

Db 375 GCTGGAACTGAACCGGAGTCTGGTGGCGGACCCCGGAGAGACATCTTCGACAGTGA 434
QY 997 CTGTATGATAGTATGTCAGAGTGTGGCGGCGCCCTGCGCCCGGAGTAACTCGGGCATCAG 1056
DB 435 CTGTATGATAGTATGTCAGAGTGTGGCGGCGCCCTGCGCCCGGAGTAACTCGGGCATCAG 494
QY 1057 CGCCAGTGTCTAGGCGAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1116
DB 495 CGCCAGTGTCTAGGCGAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 554
QY 1117 CATCGGCCACTACTACCGGGGTCTCTCTTCAGCACACGAGCAGAGCAGTG 1163
DB 555 CATCGGCCACTACTACCGGGGTCTCTCTTCAGCACACGAGCAGAGCAGTG 601

RESULT 8
AL558881/c
LOCUS
DEFINITION
  AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
  Homo sapiens cDNA clone CS0DJ015VF12 3-PRIME, mRNA sequence.
ACCESSION
  AL558881
VERSION
  AL558881.3 GI:46184268
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 850)
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  On Feb 15, 2001 this sequence version replaced gi.31283014.
  Contact: Genoscope
  Genoscope - Centre National de Séquençage
  2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with NotI and cloned
  into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen. This sequence belongs to sequence cluster
  9945.r
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?s=CS0DJ015DC06NP1&c=9945.r.
FEATURES
  source
    1..850
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0DJ015VF12"
    /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
    /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
    10-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with NotI and EcoR V sites of the NotI and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
  Query Match 40.3%; Score 533; DB 1; Length 850;
  Best Local Similarity 99.5%; Pred. No. 2.4e-251;
  Matches 733; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 585 TCAGTGTCTCTGAGCCACTACAAAGTGTGTGACGGTCTTTCATCAGCGGACAGCC 644
DB 846 TCAGTGTCTCTGAGCCACTACAAAGTGTGTGACGGTCTTTCATCAGCGGACAGCC 787
QY 645 AGGGCGGAGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTTCGAGAGCA 704
DB 786 AGGGCGGAGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTTCGAGAGCA 727

```


QY 1214 CCCTAGAGAGCGAGCCATCTCGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 1273
|||||
Db 388 CCCTAGAGAGCGAGCCATCTCGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 447
|||||
QY 1274 TAGGGTCCCCAGGGGGCCCGGGCTGGGGCTGCGGTAGGTGAAAGGCAG 1321
|||||
Db 448 TAGGGTCCCCAGGGGGCCCGGGCTGGGGCTGCGGTAGGTGAAAGGCAG 495
|||||

RESULT 15
BU859860
LOCUS
DEFINITION AGENECOURT 10442713 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6650839 5', mRNA sequence.
ACCESSION BU859860
VERSION BU859860.1 GI:24044852
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 964)
NTH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2896 row: 1 column: 07
High quality sequence stop: 613.
Location/Qualifiers
1. .964
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6650839"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 34.1%; Score 450; DB 5; Length 964;
Best Local Similarity 100.0%; Pred. No. 2.1e-210;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 872 GACGGGAGAGAGCCCCACCTACAGGGGCGCTGACACCTCCAGCTTCGGGACCCCGAG 931
|||||
Db 35 GACGGGAGAGAGCCCCACCTACAGGGGCGCTGACACCTCCAGCTTCGGGACCCCGAG 94
|||||
QY 932 CAGCAGCTGGAACGTGAACCGGAGTCGGTGGCGCACCCCAACAGAACCATCTTCGAC 991
|||||
Db 95 CAGCAGCTGGAACGTGAACCGGAGTCGGTGGCGCACCCCAACAGAACCATCTTCGAC 154
|||||
QY 992 AGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCCCCCAGCACTTCGGGC 1051
|||||
Db 155 AGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCCCCCAGCACTTCGGGC 214
|||||
QY 1052 ATCAGGCCACGTCGTACGGCAGCGGGGGCGCATGGAGGGGCGCGCCACCTACAGC 1111
|||||

Search completed: February 19, 2005, 23:58:32
Job time : 4159.91 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 06:35:20 ; Search time 3714.3 Seconds
(without alignments)
11232.262 Million cell updates/sec

Title: US-09-934-249-3
Perfect score: 861
Sequence: 1 atgcaccgttgatgggggt.....aacagaaaggacaccctctc 861

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : GenEmbl.*
- 1: gb_ba.*
 - 2: gb_hgt.*
 - 3: gb_in.*
 - 4: gb_cm.*
 - 5: gb_ov.*
 - 6: gb_pat.*
 - 7: gb_ph.*
 - 8: gb_pl.*
 - 9: gb_pr.*
 - 10: gb_ro.*
 - 11: gb_sts.*
 - 12: gb_sy.*
 - 13: gb_un.*
 - 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	861	100.0	861 6 AX392419 Sequence
2	861	100.0	1321 6 AX392417 Sequence
3	861	100.0	4839 6 CQ812357 Sequence
4	861	100.0	4839 6 AF305616 Homo sapi
5	859.4	99.8	1383 6 AX775889 Sequence
6	839.4	97.5	1061 9 BC015918 Homo sapi
7	755.2	87.7	969 6 BD272494 Secretd
8	754.2	87.6	1141 9 AF224278 Homo sapi
9	753.8	87.5	1913 6 BD272544 Secretd
10	753.6	87.5	969 6 BD272514 Secretd
11	753.6	87.5	969 6 BD272515 Secretd
12	753.6	87.5	969 6 BD272516 Secretd
13	753.6	87.5	1140 6 AR336830 Sequence
14	752.8	87.4	759 6 AR336831 Sequence
15	752.6	87.4	1085 6 AX775887 Sequence
16	752.4	87.4	759 6 BD272545 Secretd
17	752	87.3	1818 9 AY128643 Homo sapi
18	751.2	87.2	756 6 BD272495 Secretd
19	750.4	87.2	753 6 BD272534 Secretd

20	749.4	87.0	1060	9	BC080635	BC080635 Homo sapi	
21	614.6	71.4	1379	10	BC036995	BC036995 Mus muscu	
22	612.4	71.1	878	6	AX392428	AX392428 Sequence	
23	597	69.3	600	6	CQ728942	CQ728942 Sequence	
24	584	67.8	895	10	BC069890	BC069890 Mus muscu	
25	564.4	65.6	1265	5	AJ720618	AJ720618 Gallus ga	
26	546.4	63.5	61505	9	AF305426	AF305426 Homo sapi	
C	27	546.4	63.5	130435	9	HS718J7	AL035541 Human DNA
28	544.4	63.2	1583	6	AX593655	AX593655 Sequence	
29	462.2	53.7	1713	6	BD272504	BD272504 Secretd	
30	461.2	53.6	651	6	BD272505	BD272505 Secretd	
31	460.6	53.5	1713	6	BD272517	BD272517 Secretd	
32	460.6	53.5	1713	6	BD272518	BD272518 Secretd	
33	460.6	53.5	1713	6	BD272519	BD272519 Secretd	
34	458.2	53.2	648	6	BD272535	BD272535 Secretd	
C	35	445.6	51.8	693	6	AX392430	AX392430 Sequence
36	421	48.9	651	10	AF220208	AF220208 Mus muscu	
37	417.4	48.5	812	6	BD226320	BD226320 Pancreat	
38	417.4	48.5	812	6	AX011709	AX011709 Sequence	
39	401.4	46.6	408	6	AX071267	AX071267 Sequence	
40	400.6	46.5	673	6	AX525744	AX525744 Sequence	
C	41	373.2	43.3	156698	10	AL837509	AL837509 Mouse DNA
42	373.2	43.3	175847	2	AC110189	AC110189 Mus muscu	
C	43	373.2	43.3	231930	2	AC134911	AC134911 Mus muscu
C	44	353.6	41.1	249554	2	AC139417	AC139417 Rattus no
45	353.6	41.1	258632	2	AC111878	AC111878 Rattus no	

ALIGNMENTS

RESULT 1
LOCUS AX392419 861 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 3 from Patent WO0216416.
ACCESSION AX392419
VERSION AX392419.1 GI:19700734
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Lee,R.T., Landschulz,K.T., Kennedy,S.P., Thompson,J.F. and
AUTHORS Turi,T.G.
TITLE Diagnosis and treatment of cardiovascular conditions
JOURNAL Patent: WO 0216416-A 3 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)
FEATURES
source
1. .861
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. .>861
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAD29006.1"
/db_xref="GI:19700735"
/translation="MRLMGVNSTAAAGQPNVCTCNKRSFOSMEITELFVQI
IIIVVMVWVYITCLSHYKLSAKSFISRHSGRRRDALSSEGLWSESTVSGN
GIPEQVYAPPPTRDLVPPFAQRERFRFQTYLPYLQHEIDLPPTLSLSDGEEPP
YQPCCTQLQDRPEQQLNRESVRAPNRTIFDLSLMDLSARLGGPCPPSSNSGISATC
YSGGRMEGPPPTYSVIGHYPGSSFQHQSSGPPSLLEGLRLHHTHIAPLESAAIWS
KEKDKQKHPL"

ORIGIN

Query Match 100.0%; Score 861; DB 6; Length 861;
Best Local Similarity 100.0%; Pred. No. 7.4e-137;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACCGTGTATGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCAATGTC 60
|||||
Db 1 ATGCACCGTGTATGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCAATGTC 60
|||||


```
Db 1133 GGGTCTCTCTTCAGACACAGAGAGAGTGGGCGCCCTCTCTTCTGGAGGGGACCCGG 1192
Qy 781 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 840
Db 1193 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 1252
Qy 841 AAACAGAAAGGACACCTCTC 861
Db 1253 AAACAGAAAGGACACCTCTC 1273

RESULT 3
C0812357
DEFINITION Sequence 109 from Patent WO2004038020.
ACCESSION C0812357
VERSION C0812357.1 GI:47601977
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Wittig, R., Poustka, A., Mollenhauer, J. and Schadendorf, D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 109 06-MAY-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)
FEATURES             Location/Qualifiers
     source            1..4839
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
     misc_feature      1..4839
                        /note="NM_020182"
ORIGIN
Query Match          100.0%; Score 861; DB 6; Length 4839;
Best Local Similarity 100.0%; Pred. No. 5.8e-137;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACCGCTTGATGGGGGTCAACAGCAGCCGCGCGCCGCGCGGGGAGCCCAATGTC 60
Db 321 ATGCACCGCTTGATGGGGGTCAACAGCAGCCGCGCGCGCGGGGAGCCCAATGTC 380
Qy 61 TCCTGCACGTGCAACTCCTCAACCGCTCTTCTTCAGAGCATGAGATCAGCGAGCTGGAG 120
Db 381 TCCTGCACGTGCAACTCCTCAACCGCTCTTCTTCAGAGCATGAGATCAGCGAGCTGGAG 440
Qy 121 TTTGTTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGC 180
Db 441 TTTGTTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGC 500
Qy 181 CTGCTGAGCCACTACAGCTGTCTGCAAGCTCTTCTTCATCAGCGGCACAGCCAGGGGCGG 240
Db 501 CTGCTGAGCCACTACAGCTGTCTGCAAGCTCTTCTTCATCAGCGGCACAGCCAGGGGCGG 560
Qy 241 AGGAGAGAAATGCTGCTCCTCAGAGAGTGGTGGGCTTCGGAGAGCAGAGTGTC 300
Db 561 AGGAGAGAAATGCTGCTCCTCAGAGAGTGGTGGGCTTCGGAGAGCAGAGTGTC 620
Qy 301 GGCAACGGAATCCAGAGCGCAGGTCTACGCGCCGCTCGCGCCACCGACCGCGCTGGCC 360
Db 621 GGCAACGGAATCCAGAGCGCAGGTCTACGCGCGCTCGCGCCACCGACCGCGCTGGCC 680
Qy 361 GTGCGCGCTTCGCGCCAGCGGAGCGCTTCCACGCTTCAGCGCCACCTATTCGTAACCTG 420
Db 681 GTGCGCGCTTCGCGCCAGCGGAGCGCTTCCACGCTTCAGCGCCACCTATTCGTAACCTG 740
Qy 421 CAGCAGAGATCGACTGCGCCACCCACCATCTCGTGTGTCAGCGGGAGGAGCCCGCCACC 480
Db 741 CAGCAGAGATCGACTGCGCCACCCACCATCTCGTGTGTCAGCGGGAGGAGCCCGCCACC 800
```

```
Qy 481 TACCAGGGGCCCTTGACCCCTCCAGCTTCGGGACCCGAGCAGAGCTGGAACTGAACCGG 540
Db 801 TACCAGGGGCCCTTGACCCCTCCAGCTTCGGGACCCGAGCAGAGCTGGAACTGAACCGG 860
Qy 541 GAGTCGGTGGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTGATGGATAGTGCC 600
Db 861 GAGTCGGTGGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTGATGGATAGTGCC 920
Qy 601 AGGCTGGGCGGCCCTTCGCCGCCCCAGCAGTAACCTCGGGCATCAGCGCACGTCGTACGGC 660
Db 921 AGGCTGGGCGGCCCTTCGCCGCCCCAGCAGTAACCTCGGGCATCAGCGCACGTCGTACGGC 980
Qy 661 AGGCGGGGGCGCATGAGGGGCGCGCCGCCCATCTACAGGAGGTCTATCGGCCATACCCG 720
Db 981 AGCGGGGGCGCATGAGGGGCGCGCGCCCATCTACAGGAGGTCTATCGGCCATACCCG 1040
Qy 721 GGGTCTCTCTTCAGCAGCAGCAGCAGTGGGCGCCCTCTCTTCTGGAGGGGACCCGG 780
Db 1041 GGGTCTCTCTTCAGCAGCAGCAGCAGTGGGCGCCCTCTCTTCTGGAGGGGACCCGG 1100
Qy 781 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 840
Db 1101 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 1160
Qy 841 AAACAGAAAGGACACCTCTC 861
Db 1161 AAACAGAAAGGACACCTCTC 1181

RESULT 4
AF305616
LOCUS Homo sapiens STAG1/PMEP1 mRNA, complete cds.
DEFINITION AF305616
ACCESSION AF305616
VERSION AF305616.1 GI:16303741
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 4839)
AUTHORS Rae, P.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
TITLE Characterization of a novel gene, STAG1/PMEP1, upregulated in
JOURNAL renal cell carcinoma and other solid tumors
MEDLINE Mol. Carcinog. 32 (1), 44-53 (2001)
PUBMED 21453682
REFERENCE 2 (bases 1 to 4839)
AUTHORS Rae, P.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane, QLD
4001, Australia
FEATURES             Location/Qualifiers
     source            1..4839
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /chromosome="20"
                        /map="20q13.2-q13.33"
                        /notes="unknown function"
                        /codon_start=1
                        /product="STAG1/PMEP1"
                        /protein_id="AA116781.1"
                        /db_xref="GI:16303742"
     CDS                321..1184
```


181 GTCTGACGGTCTTTCATCAGCGGACACAGCCAGGCGCGGAGGAGAGAGATCCCTGTG 240
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

RESULT 7
BD272494
LOCUS
DEFINITION
SECRETED proteins and nucleic acids encoding them.
ACCESSION
BD272494
VERSION
BD272494.1 GI:33082262
KEYWORDS
JP 2002539773-A/3.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 969)
Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 3 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002539773-A/3
PD 26-NOV-2002
PE 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC
GOIN33/15,

PC GOIN33/50, GOIN33/53, GOIN33/53, GOIN33/566, C12N15/00, C12N5/00 CC
Secreted proteins and nucleic acids encoding them FH Key
FT CDS Location/Qualifiers
1.969
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 87.7%; Score 755.2; DB 6; Length 969;
Best Local Similarity 99.6%; Pred. No. 7.4e-119;
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
102 GGAGTACCGGAGCTGGAGTTGTTTCAGATCATCATCTGCTGGTGTGATGATGATGAT 161
2 GGAGATGGCGGAGCTGGAGTTGTTTCAGATCATCATCTGCTGGTGTGATGATGATGAT 61
162 GGTGTGTGTGATCAGTGTCTGCTGAGCCATACAACTGTCTGCAAGCTGTCTGCAAGCTGTCTGATCAG 221
62 GGTGTGTGTGATCAGTGTCTGCTGAGCCATACAACTGTCTGCAAGCTGTCTGATCAG 121
222 CCGGACACCGGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 281
122 CCGGACACCGGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
282 CTCGGAGGAGCAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 341
182 CTCGGAGGAGCAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
342 GCCACCGGAGCTGGGCGCTGCGCGCTTGGCCGAGCGGAGCGCTTCCACCGCTTCCA 401
242 GCCACCGGAGCTGGGCGCTGCGCGCTTGGCCGAGCGGAGCGCTTCCACCGCTTCCA 301
402 GCCACCGTATCGTACCTGTCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 461
302 GCCACCGTATCGTACCTGTCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 361
462 CCGGAG 521
362 CCGGAG 421
522 GCAGCTGGAACTGAACCGGAGCTGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 581
422 GCAGCTGGAACTGAACCGGAGCTGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
582 TGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 641
482 TGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
642 CAGCGGAG 701
542 CAGCGGAG 601
702 GGTCTATCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 761
602 GGTCTATCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 661
762 CTTGTCTGGAG 821
662 CTTGTCTGGAG 721
822 CTGGAG 861
722 CTGGAG 761
RESULT 8
AF224278
LOCUS
DEFINITION
Homo sapiens PMEPAL protein (PMEPAL) mRNA, complete cds.
ACCESSION
AF224278

[illegible]


```
QY 166 GTGGTATCAGTGTGCTGAGCCACTAAGCTGTCTGACGGTCTTTCATCAGCCGG 225
Db 61 GTGGTATCAGTGTGCTGCTGAGCCACTAAGCTGTCTGACGGTCTTTCATCAGCCGG 120
QY 226 CACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCAGAAAGATGCTGTGGCCCTCG 285
Db 121 CACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCAGAAAGATGCTGTGGCCCTCG 180
QY 286 GAGAGCAGTGTACGGCAACGAAATCCAGAGCCGCGAGTGTACGGCCCGCTCGGCC 345
Db 181 GAGAGCAGTGTACGGCAACGAAATCCAGAGCCGCGAGTGTACGGCCCGCTCGGCC 240
QY 346 ACCGACGGCTGCGCTGCGCCCTTCCGACGGGGGCGCTTCCACCGCTTCCAGCCC 405
Db 241 ACCGACGGCTGCGCTGCGCCCTTCCGACGGGGGCGCTTCCACCGCTTCCAGCCC 300
QY 406 ACCTATCCGTACCTGACGACGAGATCGACCTGCGACCCACCATCTCGCTGTGACAGCGG 465
Db 301 ACCTATCCGTACCTGACGACGAGATCGACCTGCGACCCACCATCTCGCTGTGACAGCGG 360
QY 466 GAGGAGCCCCCACTACAGGGCCCTGCAACCTCCAGCTTCCGGACCCCGAGCAGCAG 525
Db 361 GAGGAGCCCCCACTACAGGGCCCTGCAACCTCCAGCTTCCGGACCCCGAGCAGCAG 420
QY 526 CTGGAACCTGAACCGGAGTCTGCTGGCGGCAACCCCAACAGAACCATCTTCGACGTGAC 585
Db 421 CTGGAACCTGAACCGGAGTCTGCTGGCGGCAACCCCAACAGAACCATCTTCGACGTGAC 480
QY 586 CTGATGGATAGTCCAGGCTGGCGGCGCTGCGCCCTGCGCCCGCAGCAGTAACCTCGGGCATCAGC 645
Db 481 CTGATGGATAGTCCAGGCTGGCGGCGCTGCGCCCTGCGCCCGCAGCAGTAACCTCGGGCATCAGC 540
QY 646 GCCACGTGTACGGCAGCGCGCGCATGAGGGGCGCGCCCGCCACCTACAGCAGGTC 705
Db 541 GCCACGTGTACGGCAGCGCGCGCATGAGGGGCGCGCCCGCCACCTACAGCAGGTC 600
QY 706 ATCGGCACTACCGGGTCTCTTCCAGCAGCAGCAGCAGTGGGGCGCCCTCTTG 765
Db 601 ATCGGCACTACCGGGTCTCTTCCAGCAGCAGCAGCAGTGGGGCGCCCTCTTG 660
QY 766 CTGGAGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGCATCTGG 825
Db 661 CTGGAGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGCATCTGG 720
QY 826 AGCAAGAGAGGATAAACAAGAGGACACCTCTC 861
Db 721 AGCAAGAGAGGATAAACAAGAGGACACCTCTC 756
```

```
RESULT 15
AX775887 LOCUS AX775887 1085 bp mRNA linear PAT 14-JUL-2003
DEFINITION Sequence 157 from Patent WO03048202.
ACCESSION AX775887
VERSION AX775887.1 GI:32693605
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Matsuda, A. and Muramatsu, S.
AUTHORS NP-kB activating gene
TITLE Patent: WO 03048202-A 157 12-JUN-2003;
JOURNAL Asahi Kasei Kabushiki Kaisha (JP)
FEATURES Location/Qualifiers
source 1..1085
/mol_type="mRNA"
/db_xref="taxon:9606"
128..886
/notes="unnamed protein product"
/contig_start=1
CDS
```

```
/protein_id="CAE11643.1"
/db_xref="GI:32693606"
/translation="MAELFVQIIIIIVMMVMVVTCLLSHYKSARSFIRHSQG
RRERDALSEGCLMPSESTVSGNIGPEQVYAPRPTDLRLAVFPFAQREPHRFQTY
PYLQHIIDLPTISLSDGBEPYQGPCTQLQRLDPQQLNRESVRAPNRTIFDSY
LMSARLGGPCPPSSNSGISATCYSGSGRMGGPPPTVSEVIGHYPGSSFQHQSSGPP
SLLEGTRLHHTHIAPILESAAIWSKDKQKQHP."

```

ORIGIN

```
Query Match 87.4%; Score 752.6; DB 6; Length 1085;
Best Local Similarity 98.2%; Pred. No. 2e-118;
Matches 761; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 87 TTTGTTCCAGAGCATCGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGT 146
Db 109 TCTCTCGCAAAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCTCGTGT 168
QY 147 GGTGATGATGTTGATGTTGTTGTTGATCAGTCCCTGTGAGCCACTTACAACTGCTGC 206
Db 169 GGTGATGATGTTGATGTTGTTGTTGATCAGTCCCTGTGAGCCACTTACAACTGCTGC 228
QY 207 ACAGTCTTTTCATCAGCCGGCACAGCCAGGGCGGAGGAGAGAGATGCTCTCTCAGA 266
Db 229 ACAGTCTTTTCATCAGCCGGCACAGCCAGGGCGGAGGAGAGAGATGCTCTCTCAGA 288
QY 267 AGATGCTGTGTCCTTCGAGAGACACAGTGTGAGGCAACGGAATCCAGAGCCGAGGT 326
Db 289 AGATGCTGTGTCCTTCGAGAGACACAGTGTGAGGCAACGGAATCCAGAGCCGAGGT 348
QY 327 CTAGCGCCCGCTCGGCGCCACAGCCGCTGGCGCTGGCGCTGGCGCTGGCGCGGAGCG 386
Db 349 CTAGCGCCCGCTCGGCGCCACAGCCGCTGGCGCTGGCGCTGGCGCGGAGCG 408
QY 387 CTTCACACCGCTTCACGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 446
Db 409 CTTCACACCGCTTCACGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 468
QY 447 CATCTCGTGTACAGCGGGAGAGCCGCCACCTTACGAGGGCCCTTGACCTCTCAGCT 506
Db 469 CATCTCGTGTACAGCGGGAGAGCCGCCACCTTACGAGGGCCCTTGACCTCTCAGCT 528
QY 507 TCGGAGCCCGGACGACGCTGGAACCTGAACCGGGAGTGGTGGCGGACCCCAACACAG 566
Db 529 TCGGAGCCCGGACGACGCTGGAACCTGAACCGGGAGTGGTGGCGGACCCCAACACAG 588
QY 567 AACCATCTTCGACAGTGACCTGATGATAGTGCAGGCTGGCGGCGCCCTTGCCCGCCAG 626
Db 589 AACCATCTTCGACAGTGACCTGATGATAGTGCAGGCTGGCGGCGCCCTTGCCCGCCAG 648
QY 627 CAGTAACTCGGGCATCAGGCCACAGTGTCTACGCGAGCGCGGCGGCGATGAGGGCGCGCC 686
Db 649 CAGTAACTCGGGCATCAGGCCACAGTGTCTACGCGAGCGCGGCGGCGATGAGGGCGCGCC 708
QY 687 GCCACCTACAGCGAGTTCATCGGCCACTTACCGGGGCTCTCTTCCAGCAGCAGCAGAG 746
Db 709 GCCACCTACAGCGAGTTCATCGGCCACTTACCGGGGCTCTCTTCCAGCAGCAGCAGAG 768
QY 747 CAGTGGCGCGCTCTCTTCTGAGGGGACCCGGCTCCACACACACACATCGCGCCCT 806
Db 769 CAGTGGCGCGCTCTCTTCTGAGGGGACCCGGCTCCACACACACACATCGCGCCCT 828
QY 807 AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTC 861
Db 829 AGAGAGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTC 883
```

Search completed: February 19, 2005, 14:21:13.
Job time : 3716.3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 00:48:19 ; Search time 460.884 Seconds
(without alignments)
11058.969 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcaccgttgatgggggt.....aacagaaaggacacctctc 861

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861	100.0	864	11	Adn38809 Cancer/an
2	861	100.0	1321	6	Abk12137 Human cdn
3	861	100.0	4839	8	Acc49552 Tumour-as
4	861	100.0	4839	11	Adp65809 Human STA
5	861	100.0	4839	11	Adp65729 Human tra
6	861	100.0	4839	12	Adm67045 Human hom
7	861	100.0	4839	13	Adr65875 Human pro
8	861	100.0	4839	13	Adr66778 Human pro
9	861	100.0	4911	13	Acn40804 Tumour-as
10	859.4	99.8	1383	10	Adc37326 Nuclear f
11	755.2	87.7	969	3	Aaa75151 cDNA enco
12	754.2	87.6	1140	6	Abk92120 Prostate
13	754.2	87.6	1141	10	Adb75588 Prostate
14	754.2	87.6	1850	8	Acc49536 Tumour-as
15	754.2	87.6	4527	11	Adl83313 Human and
16	753.6	87.5	969	3	Aaa75164 cDNA clon
17	753.6	87.5	969	3	Aaa75163 cDNA clon
18	753.6	87.5	969	3	Aaa75165 cDNA clon
19	753.6	87.5	1140	10	Adb60105 Human and
20	753.6	87.5	1140	10	Adh62276 Human PME

21	753.6	87.5	1140	12	Ado39826
22	752.8	87.4	759	10	Adf17545
23	752.8	87.4	759	10	Adh62277
24	752.8	87.4	759	12	Ado39827
25	752.6	87.4	806	8	Acc49537
26	752.6	87.4	1061	3	Aaa47429
27	752.6	87.4	1085	10	Adc37324
28	752.6	87.4	1334	8	Abz36103
29	742.4	86.2	1066	4	Aai57868
30	712	82.7	1069	4	Aai59654
31	612.4	71.1	878	6	Abk12142
32	544.4	63.2	1583	6	Abse61424
33	462.2	53.7	1713	3	Aaa75152
34	460.6	53.5	1713	3	Aaa75167
35	460.6	53.5	1713	3	Aaa75166
36	445.6	51.8	693	6	Abk12143
37	445.6	51.8	693	6	Abk12143
38	417.4	48.5	812	2	Aaz52964
39	417	48.4	474	10	Abz84732
40	401.4	46.6	408	5	Aaf65983
41	400.6	46.5	673	6	Abt09178
42	400.6	46.5	673	12	Adg45576
43	400.6	46.5	673	12	Adh22874
44	352.2	40.9	8018	11	Acn44959
45	352.2	40.9	8494	5	Aas77304

ALIGNMENTS

RESULT 1

ADN38809

ID ADN38809 standard; cDNA; 864 BP.

XX

AC ADN38809;

XX

DT 17-JUN-2004 (first entry)

XX

DE

XX

KW

KW

KW

KW

KW

KW

KW

OS

XX

XX

PN

XX

XX

PD

XX

XX

PF

XX

XX

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:127.

Human; differential expression; cancer; angiogenic disorder;

fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

inflammatory disease; autoimmune disease;

retinal neovascularisation syndrome; scarring; uterine fibroid;

detection; diagnosis; prognosis; drug screening; drug targeting;

wound healing; contraception; cytostatic; cardiant; immunomodulatory;

vulnerary; gene therapy; vaccine; gene; ss.

Homo sapiens.

WO2003042661-A2.

22-MAY-2003.

13-NOV-2002; 2002WO-US036810.

13-NOV-2001; 2001US-0350666P.

21-NOV-2001; 2001US-0332464P.

29-NOV-2001; 2001US-0334393P.

03-DEC-2001; 2001US-0335394P.

14-DEC-2001; 2001US-0340376P.

08-JAN-2002; 2002US-0347211P.

10-JAN-2002; 2002US-0347349P.

08-FEB-2002; 2002US-035250P.

13-FEB-2002; 2002US-0356714P.

20-FEB-2002; 2002US-0359077P.

09-MAR-2002; 2002US-036809P.

04-APR-2002; 2002US-0370110P.

12-APR-2002; 2002US-0372246P.

05-JUN-2002; 2002US-0386614P.

16-JUL-2002; 2002US-0396839P.

22-JUL-2002; 2002US-0397775P.

22-JUL-2002; 2002US-0397845P.

Db	1133	GGGTCTCTCTCCAGCAGCAGACAGTGGCGCGCCCTCCTTGTGTGAGGGGACCCGG	1192
Qy	781	CTTCACGACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGAGCAAGAGAGAGAT	840
Db	1193	CTTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGAGCAAGAGAGAGAT	1252
Qy	841	AAACAGAAAGGACACCTCTC	861
Db	1253	AAACAGAAAGGACACCTCTC	1273

RESULT 3	
ACC49552	
ID	ACC49552 standard; cDNA; 4839 BP.
XX	
XX	
AC	ACC49552;
XX	
XX	
DT	01-JUL-2003 (first entry)
XX	
XX	
DE	Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.
XX	
KW	Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
KW	cancer; gene; ss.
XX	
XX	
OS	Homo sapiens.
XX	
PN	WO2003024392-A2.
XX	
PD	27-MAR-2003.
XX	
XX	
PF	11-SEP-2002; 2002WO-US028859.
XX	
XX	
PR	18-SEP-2001; 2001US-0323368P.

(GETH) GENENTECH INC.

Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
Williams PM, Wu TD, Zhang Z;
WPI; 2003-354551/33.
P-PSDB; ABP97234.

New antibodies against tumor-associated antigenic target polypeptide,
useful for treating or diagnosing tumors or cancers in mammals, e.g.
prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
carcinomas.

Claim 2; Fig 119; 285pp; English.

ACC49493 to ACC49552 encode the human tumour-associated antigenic target
(TAT) proteins given in ABP97175 to ABP97234. The present invention
describes an isolated antibody that binds to a polypeptide having at
least 80 % sequence identity to any of the 60 150-800 residue amino acid
sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
its associated signal peptide, encoded by any of the 60 2000-3000 base
pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
cytostatic activity. The antibody can be used for treating or diagnosing
tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
cell carcinomas, or thyroid cancer

Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
Query Match 100.0%; Score 861; DB 8; Length 4839;
Best Local Similarity 100.0%; Pred. No. 2.9e-167;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	841	AAACAGAAAGGACACCCCTCTC	861
Db	1161	AAACAGAAAGGACACCCCTCTC	1181
RESULT 9			
ACN40804	ACN40804 standard; cDNA; 4911 BP.		
XX	AC	ACN40804;	
XX	DT	18-NOV-2004 (first entry)	
XX	DE	Tumour-associated antigenic target (TAT) cDNA DNA326860, SEQ ID NO:5823.	
XX	KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;	
XX	KW	tumour; diagnosis; cell proliferative disorder; breast cancer;	
XX	KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;	
XX	KW	central nervous system cancer; bladder cancer; pancreatic cancer;	
XX	KW	cervical cancer; melanoma; leukaemia; hybridisation probe;	
XX	KW	chromosome identification; chromosome mapping; gene mapping;	
XX	OS	gene therapy; cytosstatic; gene; ss.	
XX	OS	Homo sapiens.	
XX	PN	WO2004030615-A2.	
XX	PD	15-APR-2004.	
XX	XX	29-SEP-2003; 2003WO-US028547.	
XX	PF	02-OCT-2002; 2002US-0414971P.	
XX	PR	(GETH) GENENTECH INC.	
XX	PA	Wu TD, Zhang Z, Zhou Y;	
XX	PI	WPI; 2004-347921/32.	
XX	XX	New tumor-associated antigenic target polypeptides and nucleic acids,	
XX	PT	useful in preparing a medicament for treating or detecting a	
XX	PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or	
XX	PT	prostate cancer or tumor.	
XX	PS	Claim 1; SEQ ID NO 5823; 7273pp; English.	
XX	CC	The invention relates to human tumour-associated antigenic target (TAT)	
XX	CC	polypeptides, and their related nucleic acids. The TAT polypeptides are	
XX	CC	overexpressed in cancer tissues compared to normal tissues, and may thus	
XX	CC	serve as effective targets for the diagnosis and treatment of cancer in	
XX	CC	mammals. The invention also relates to nucleic acid and polypeptide	
XX	CC	sequences at least 80% identical to the TAT nucleic acids and	
XX	CC	polypeptides; expression vectors and host cells comprising a TAT nucleic	
XX	CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic	
XX	CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a	
XX	CC	TAT polypeptide; and methods and compositions for the treatment or	
XX	CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,	
XX	CC	antibodies, antagonists, binding molecules and compositions are useful	
XX	CC	for diagnosing or treating a cell proliferative disorder associated with	
XX	CC	increased TAT expression, particularly cancers such as breast cancer,	
XX	CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder	
XX	CC	cancer, pancreatic cancer, cervical cancer, cancers of the central	
XX	CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be	
XX	CC	used as hybridisation probes, in chromosome and gene mapping, in	
XX	CC	chromosome identification and in gene therapy. The present sequence	
XX	CC	represents a TAT nucleic acid of the invention	
XX	XX	Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;	
Query Match 100.0%; Score 861; DB 13; Length 4911;			
Best Local Similarity 100.0%; Pred. No. 3e-167;			
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

PA (MILL-) MILLENNIUM PHARM INC.
 XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
 PI WPI; 2000-579269/54.
 DR P-PSDB; AABI8449.
 DR Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 PT treating cancer.
 PS Claim 2; Fig 5; 175pp; English.
 XX The present sequence encodes a human TANGO 261 polypeptide. The
 CC specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
 CC 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate cellular
 CC adhesion. The proteins can be used to treat any von Willebrand factor-
 CC associated disorder, regulate extracellular matrix structuring, cellular
 CC adhesion, and cell trafficking and/or migration, modulate cellular
 CC interactions, modulate cell adhesion in proliferative disorders, such as
 CC cancer, modulate the proliferation, differentiation, and/or function of
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 CC blood and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to treat
 CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders
 XX
 SQ Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;

Query Match 87.7%; Score 755.2; DB 3; Length 969;
 Best Local Similarity 99.6%; Pred. No. 1.3e-145;
 Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 102 GGAGATACGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGTGAT 161
 DB 2 GGAGATGGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGTGAT 61
 QY 162 GGTGGTGTGATCATCGTCTGCTGAGCCACTACAGTCTGTCAGGTCCTTCATCAG 221
 DB 62 GGTGGTGTGATCATCGTCTGCTGAGCCACTACAGTCTGTCAGGTCCTTCATCAG 121
 QY 222 CCGGCACAGCCAGGGCGGAGGAGAGAGATGCCCTGTCTCAGAAAGGATGCCCTGTGGCC 281
 DB 122 CCGGCACAGCCAGGGCGGAGGAGAGAGATGCCCTGTCTCAGAAAGGATGCCCTGTGGCC 181
 QY 282 CTGCGAGAGACAGTGTTCAGGCAACGGAATCCAGAGCCGACGGTCTACGCCCCCGCTCG 341
 DB 182 CTGCGAGAGACAGTGTTCAGGCAACGGAATCCAGAGCCGACGGTCTACGCCCCCGCTCG 241
 QY 342 GCCCAGCGAGCCGCTGGCGGTGGCGCCCTTCGCCCGGAGGCGCTTCACCGCTTCCA 401
 DB 242 GCCCAGCGAGCCGCTGGCGGTGGCGCCCTTCGCCCGGAGGCGCTTCACCGCTTCCA 301
 QY 402 GCCCAGCTATCCCTGCTGAGCAGCAGATCGACCTGCCACCCACCATCTCGTGTGAGA 461
 DB 302 GCCCAGCTATCCCTGCTGAGCAGCAGATCGACCTGCCACCCACCATCTCGTGTGAGA 361
 QY 462 CGGGAGGAGCCGCCACCTTACAGGGCCCTTGCACCTTCAGCTTCGGGACCCCGAGCA 521
 DB 362 CGGGAGGAGCCGCCACCTTACAGGGCCCTTGCACCTTCAGCTTCGGGACCCCGAGCA 421
 QY 522 GCAGCTGGAACCTAACCGGAGTCTGGCGGACCCCGGAGCAACCACTCTTCACAG 581
 DB 422 GCAGCTGGAACCTAACCGGAGTCTGGCGGACCCCGGAGCAACCACTCTTCGACAG 481

QY 582 TGACCTGATGGATAGTGTCCAGGGCTGGCGGGCCCTGCCCCCCCCCAGCAGTAACCTCGGCGCAT 641
 DB 482 TGACCTGATGGATAGTGTCCAGGGCTGGCGGGCCCTGCCCCCCCCCAGCAGTAACCTCGGCGCAT 541
 QY 642 CAGCGCCACGTGTCTACGGCAGCGGGCGGCATGGAGGGGGCCCGCCACCTACACGCA 701
 DB 542 CAGCGCCACGTGTCTACGGCAGCGGGCGGCATGGAGGGGGCCCGCCACCTACACGCA 601
 QY 702 GGTTCATCGGCCACTACCCCGGGGTCTCTTCCAGCACCAGCAGAGCAGTGGCGCGCCCTC 761
 DB 602 GGTTCATCGGCCACTACCCCGGGGTCTCTTCCAGCACCAGCAGAGCAGTGGCGCGCCCTC 661
 QY 762 CTTGCTGGAGGGAGCCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGGAGCGCAT 821
 DB 662 CTTGCTGGAGGGAGCCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGGAGCGCAT 721
 QY 822 CTGGACCAAGAGAGAGGATTAACAGAAAGGACACCCCTCTC 861
 DB 722 CTGGACCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 761

RESULT 12
 ABK92120
 ID ABK92120 standard; DNA; 1140 BP.
 XX
 AC ABK92120;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Prostate cancer-associated DNA sequence #6.
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 KW gene therapy; gene; ds.
 XX
 OS Mammalia.
 XX
 FN WO200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 XX 12-OCT-2001; 2001WO-US032045.
 XX
 XX 13-OCT-2000; 2000US-00687576.
 PR 08-DEC-2000; 2000US-00733288.
 PR 08-DEC-2000; 2000US-00733742.
 PR 24-JAN-2001; 2001US-0263957P.
 PR 16-MAR-2001; 2001US-0276791P.
 PR 16-MAR-2001; 2001US-0276888P.
 PR 06-APR-2001; 2001US-0281922P.
 PR 24-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0288589P.
 XX
 PA (BOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX
 DR WPI; 2002-471335/50.
 DR P-PSDB; ABG61805.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 22; Page 305; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridise to a sequence that is at least 80% identical to them. The

prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. ABR92115-ABR92263 represent prostate cancer-associated polynucleotide sequences

SQ Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

Query Match	87.6%	Score 754.2;	DB 6;	Length 1140;
Best Local Similarity	98.3%	Pred. No. 2.1e-145;		
Matches 762;	Conservative	0;	Mismatches 13;	Indels 0;
Gaps 0;				

87	QY	TTTGTTCAGAGCATGGAGATCA	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT	146
77	Db			136
		TTCTCTCGGAAAC	CAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT	
147	QY	GGTGATGATGGTGATGCTGGTGATCA	CGTGTCTGCTGAGCCACTACAAGAGCTGTCTGC	206
137	Db			196
		GGTGATGATGGTGATGCTGGTGATCA	CGTGTCTGCTGAGCCACTACAAGAGCTGTCTGC	
207	QY	ACGGTCTTCATCAGCCCGGCAC	ACGAGGGCGGAGGAGAGAGATGCCCTGTCTCTCAGA	266
197	Db			256
		ACGGTCTTCATCAGCCCGGCAC	ACGAGGGCGGAGGAGAGAGATGCCCTGTCTCTCAGA	
267	QY	AGGATGCTGTGGCCCTTCGAGAGCA	CAGTGTCTAGGCAACGGAAATCCAGAGCCGCAGGT	326
257	Db			316
		AGGATGCTGTGGCCCTTCGAGAGCA	CAGTGTCTAGGCAACGGAAATCCAGAGCCGCAGGT	
327	QY	CTACGCCCCGCTCGGCCAC	CCGACCGCTGGCCGTGCGCCCTTCGCCCAGCCGGAGCG	386
317	Db			376
		CTACGCCCCGCTCGGCCAC	CCGACCGCTGGCCGTGCGCCCTTCGCCCAGCCGGAGCG	
387	QY	CTTCCACCGCTTCAGCCCCACTAT	CTCGTACTCTCAGCACGAGATCGACCTGCCACCCAC	446
377	Db			436
		CTTCCACCGCTTCAGCCCCACTAT	CTCGTACTCTCAGCACGAGATCGACCTGCCACCCAC	
447	QY	CATCTCTGTCTCAGACGGGAGAG	CCCCCACTTACGAGGCCCTTCGCACTCTCGAGCT	506
437	Db			496
		CATCTCTGTCTCAGACGGGAGAG	CCCCCACTTACGAGGCCCTTCGCACTCTCGAGCT	
507	QY	TCGGGACCCGAGCAGCAGCT	TGGAACTGAACCGGGAGTTCGGTCGGCGCACCCCCAAACAG	566
497	Db			556
		TCGGGACCCGAGCAGCAGCT	TGGAACTGAACCGGGAGTTCGGTCGGCGCACCCCCAAACAG	
567	QY	AACCATCTTCGACAGTGACCT	TGATGGATAGTGCAGGCTGGGGCGGCCCTTCGCCCCCCAC	626
557	Db			616
		AACCATCTTCGACAGTGACCT	TGATGGATAGTGCAGGCTGGGGCGGCCCTTCGCCCCCCAC	
627	QY	CAGTAACTCGGGCATCAGCCGC	ACGTGCTACGGCAGCGGGCGGCATAGAGGGGCGGCC	686
617	Db			676
		CAGTAACTCGGGCATCAGCCGC	ACGTGCTACGGCAGCGGGCGGCATAGAGGGGCGGCC	
687	QY	GCCCACTACAGCGAGGTCACT	CGGCCACTACCGGGGTCTCTTCTTCAGCACACGACGAG	746
677	Db			736
		GCCCACTACAGCGAGGTCACT	CGGCCACTACCGGGGTCTCTTCTTCAGCACACGACGAG	
747	QY	CAGTGGGCGGCCCTCTCTT	GCTGGAGGGGACCCCGGCTCCACACACATCGCGCCCT	806
737	Db			796
		CAGTGGGCGGCCCTCTCTT	GCTGGAGGGGACCCCGGCTCCACACACATCGCGCCCT	
807	QY	AGAGCGGAGCCATCTGGAGCA	AAAGAGGATAAACAGAAAGGACACCCCTCTC	861
797	Db			851
		AGAGCGGAGCCATCTGGAGCA	AAAGAGGATAAACAGAAAGGACACCCCTCTC	

RESULT 13
ADB75588

ID	ADB75588 standard; cDNA; 1141 BP.
XX	
AC	ADB75588;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Prostate cancer marker cDNA.
XX	
KW	Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX	
OS	Homo sapiens.
XX	
PN	W02003009814-A2.
XX	
PD	06-FEB-2003.
XX	
PF	25-JUL-2002; 2002WO-US023913.
XX	
PR	25-JUL-2001; 2001US-0307982P.
PR	22-AUG-2001; 2001US-0314356P.
PR	25-SEP-2001; 2001US-0325020P.
PR	12-DEC-2001; 2001US-0341746P.
PR	05-MAR-2002; 2002US-0362158P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI	Hoern S, Kamatkar S, Wonsey AM, Ghatt K, Zhao X, Anderson D;
XX	
DR	WPI; 2003-248033/24.
XX	
XX	New nucleic acid molecule, useful for diagnosing or treating prostate
PT	cancer.

Sequence 1141 BP; 271 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

Query Match	87.6%	Score 754.2;	DB 10;	Length 1141;
Best Local Similarity	98.3%;	Pred. No. 2.1e-145;		
Matches 762;	Conservative	0;	Mismatches 13;	Indels 0;
Gaps	0;			

87	TTTGTTCAGAGCATGGAGATCA	CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT	146	
Qy				
Db	77	TCTCTGCGAAACAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT	136	
Qy	147	GGTGATGATGCTGATGGTGGTGATCA	CGTGCCCTCTGAGCCACTACAAGCTGTCCTC	206
Db	137	GGTGATGATGCTGATGGTGGTGATCA	CGTGCCCTCTGAGCCACTACAAGCTGTCCTC	196
Qy	207	ACGGTCTTTCATCAGCCGGGACAGCCAGGGGCGGAGGAGAGAAGATGC	CCCTGTCTCTCAGA	266
Db	197	ACGGTCTTTCATCAGCCGGGACAGCCAGGGGCGGAGGAGAGAAGATGC	CCCTGTCTCTCAGA	256
Qy	267	AGGATGCTGTGGCCCTCGGAGAGCA	CAGTGTTCAGGCCAACGGAAATCCCGAGCCGAGGT	326
Db	257	AGGATGCTGTGGCCCTCGGAGAGCA	CAGTGTTCAGGCCAACGGAAATCCCGAGCCGAGGT	316

Qy	327	CTA	CGCCCCGGCTTCGGCCCA	CCGA	CCGCTCGCGCTGCGCCCTTCGCCACGCGGAGCG	386	
Db	317	CTA	CGCCCCGGCTTCGGCCCA	CCGAC	CGCTCGCGCTTCGCCACGCGGAGCG	376	
Qy	387	CTT	CCACCGCTTCCAGCCCA	CCCTAT	TCGTA	CTGCGACAGATCGACCTGCACCCAC	446
Db	377	CTT	CCACCGCTTCCAGCCCA	CCCTAT	TCGTA	CTGCGACAGATCGACCTGCACCCAC	436
Qy	447	CAT	CTCGTGTGACGCGGGAGG	CCCCCA	CCCTAC	CAGGCGCCTGCACCTCCAGCT	506
Db	437	CAT	CTCGTGTGACGCGGGAGG	CCCCCA	CCCTAC	CAGGCGCCTGCACCTCCAGCT	496
Qy	507	TCGGG	ACCCCGACGACGACTGGA	ACTGAA	CCGGGAGTCGGT	CGCGGCAACCCCAACAG	566
Db	497	TCGGG	ACCCCGACGACGACTGGA	ACTGAA	CCGGGAGTCGGT	CGCGGCAACCCCAACAG	556
Qy	567	AAC	CATCTTTCGACAGTACCT	GATGGAT	AGTGC	CAGGCTGGCGGCGCCCTGCCGCCACG	626
Db	557	AAC	CATCTTTCGACAGTACCT	GATGGAT	AGTGC	CAGGCTGGCGGCGCCCTGCCGCCACG	616
Qy	627	CAGTAA	CTCGGCA	TCAGCGCA	CCGTGT	CTACGGCAGCGCGCGGCGATGGAGGGCGCGCC	686
Db	617	CAGTAA	CTCGGCA	TCAGCGCA	CCGTGT	CTACGGCAGCGCGCGGCGATGGAGGGCGCGCC	676
Qy	687	GCC	CACCTACGCGAGGT	CATCGGCCA	CTAC	CCGGGGTCTCTCTTCCAGCACGACGACAG	746
Db	677	GCC	CACCTACGCGAGGT	CATCGGCCA	CTAC	CCGGGGTCTCTCTTCCAGCACGACGACAG	736
Qy	747	CAGTGGG	CGGCCCTCTT	TGCTGGAGGG	ACCGGCT	TCACACACACATCGCGCCCT	806
Db	737	CAGTGGG	CGGCCCTCTT	TGCTGGAGGG	ACCGGCT	TCACACACACATCGCGCCCT	796
Qy	807	AGAGAGCG	CAGCCATCTCGGAG	CAAGAGAT	ATAACAGAA	AGGACACCTCTC	861
Db	797	AGAGAGCG	CAGCCATCTCGGAG	CAAGAGAGAT	ATAACAGAA	AGGACACCTCTC	851

RESULT 14

ACC49536	standard; cDNA; 1850 BP.
XX	
XX	
AC	ACC49536;
XX	
XX	
DT	01-JUL-2003 (first entry)
XX	
XX	Tumour-associated antigenic target protein TAT180 cDNA SEQ ID NO:44.
XX	
KW	Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
KW	cancer; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO2003024392-A2.
XX	
XX	
PD	27-MAR-2003.
XX	
XX	
PF	11-SEP-2002; 2002WO-US028859.
XX	
PR	18-SEP-2001; 2001US-0323268P.
PR	19-OCT-2001; 2001US-0339227P.
PR	07-NOV-2001; 2001US-0336827P.
PR	20-NOV-2001; 2001US-0331906P.
PR	02-JAN-2002; 2002US-0345444P.
PR	03-APR-2002; 2002US-0369724P.
PR	19-AUG-2002; 2002US-0404809P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
PI	Williams PM, Wu TD, Zhang Z;
XX	
DR	WPI; 2003-354551/33.

Db 737 CAGTGGCGCCCTCTCTTCTGGAGGGACCGGGTCCACACACACATCGGCGCCCT 796
QY 807 AGAGAGCCGAGCATCTCGAGCAAGAGAGATAAACAGAAAGGACACACCTCTC 861
Db 797 AGAGAGCCGAGCATCTCGAGCAAGAGAGATAAACAGAAAGGACACACCTCTC 851

RESULT 15
ADL83313
ID ADL83313 standard; cDNA; 4527 BP.
XX ADL83313;
XX 20-MAY-2004 (first entry)
XX Human androgen responsive prostate specific nucleic acid, ARP2.
DE
DE
XX Human; ss; gene; androgen responsive prostate specific; ARP2;
KW prostate cancer; prostate pathology; benign prostatic hyperplasia;
KW prostatitis; prostatic neoplasm.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 96..854
FT /*tag= a
FT /product= "ARP2"
FT misc_feature 1128..4509
FT /*tag= b
FT /note= "Claimed in claim 10"
XX
XX US2003166520-A1.
XX
XX 04-SEP-2003.
XX
XX 28-MAR-2001; 2001US-00821812.
XX
XX 28-MAR-2001; 2001US-00821812.
XX (L1NB/) LIN B.
XX Lin B;
XX WPI; 2003-898096/82.
XX P-PSDB; ADL83314.
XX
XX New substantially pure androgen responsive prostate specific nucleic acid
XX molecules and polypeptides, useful for diagnosing, preventing and
XX treating prostate cancer or other prostatic pathologies, e.g.
XX prostatitis.
XX
XX Claim 9; SEQ ID NO 2; 43pp; English.
XX
XX The invention relates to a substantially pure androgen responsive
XX prostate specific (ARP) nucleic acid molecule selected from ARP1-ARP5
XX (appearing as ADL83312, ADL83313, ADL83314, ADL83315, ADL83316 and ADL83317). Also
XX included are methods of diagnosing or predicting susceptibility to a
XX prostate neoplastic condition in an individual, methods for treating or
XX reducing the severity of a prostate neoplastic condition in an
XX individual, a substantially pure ARP3, ARP4 or ARP5 polypeptide (or their
XX fragments, encoded by the above ARP3, ARP4 or ARP5 polypeptide (or their
XX respectively) and a binding agent comprising a molecule that selectively
XX binds the above ARP3, ARP4 or ARP5 polypeptide. The nucleic acid
XX molecules and polypeptides are useful in diagnosing, preventing and
XX treating prostate cancer or other prostate pathologies such as benign
XX prostatic hyperplasia or prostatitis. The nucleic acid molecules are used
XX as hybridisation probes in various diagnostic procedures. The present
XX sequence is the ARP2 cDNA.
XX
XX Sequence 4527 BP; 1089 A; 1149 C; 1175 G; 1113 T; 0 U; 1 Other;

Query Match 87.6%; Score 754.2; DB 11; Length 4527;
Best Local Similarity 98.3%; Pred. No. 2.5e-145;

Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 87 TTTGTTTCAGAGCATGAGATCAAGAGCTGGAGTTTGTTCAGATCATCATCATCTGTTGT 146
Db 77 TCTCTCGCAAAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCATCTGTTGT 136
QY 147 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 206
Db 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
QY 207 ACGGTCTTTTCATCAGCGGCGACAGCGGCGGAGAGAGAGATGCTCTCTCTCAGA 266
Db 197 ACGGTCTTTTCATCAGCGGCGACAGCGGCGGAGAGAGAGATGCTCTCTCTCAGA 256
QY 267 AGGATGCTGTGCT 326
Db 257 AGGATGCTGTGCT 316
QY 327 CTACGCGCGCGCTCTGCGCCACCGAGCGCTGCGCGCGCTCTGCGCGCGCGCGCGCG 386
Db 317 CTACGCGCGCGCTCTGCGCCACCGAGCGCTGCGCGCGCTCTGCGCGCGCGCGCG 376
QY 387 CTTCACACCGCT 446
Db 377 CTTCACACCGCT 436
QY 447 CATCTCGCTGTGAGCGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 506
Db 437 CATCTCGCTGTGAGCGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 496
QY 507 TCGGGACCGCGGAGCGAGCTGGAATGAAACCGGAGTGGTGCGCGCACCGCGCGCGCG 566
Db 497 TCGGGACCGCGGAGCGAGCTGGAATGAAACCGGAGTGGTGCGCGCACCGCGCGCG 556
QY 567 AACCATTTTCGACAGTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 626
Db 557 AACCATTTTCGACAGTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 616
QY 627 CAGTAACTCGGCGCATCAGCGCCACCGTGTACGGCAGCGCGCGCGCGCGCGCGCGCG 686
Db 617 CAGTAACTCGGCGCATCAGCGCCACCGTGTACGGCAGCGCGCGCGCGCGCGCGCG 676
QY 687 GCCCACCTTACAGCGAGGTGATCGGCCACTTACCGCGGGTCTCTCTCTCTCTCTCTCT 746
Db 677 GCCCACCTTACAGCGAGGTGATCGGCCACTTACCGCGGGTCTCTCTCTCTCTCTCT 736
QY 747 CAGTGGCGCGCGCT 806
Db 737 CAGTGGCGCGCGCT 796
QY 807 AGAGAGCGCAGGCATCTCGAGCAAGAGAGATAAACAGAAAGGACACACCTCTCTC 861
Db 797 AGAGAGCGCAGGCATCTCGAGCAAGAGAGATAAACAGAAAGGACACACCTCTCTC 851

Search completed: February 19, 2005, 11:44:06
Job time : 462.884 secs

331	DB		GGCCACCGACCGCTTGGCGGTGGCCGCTTTCGCCAGCGGGAGCGCTTCCACCGCTTCCA	390
402	QY		GCCCACTTATCCGTACTGTGACGACGAGATGCACTTGCCACCGCACCATCTCGCTGTGAGA	461
391	DB		GGCCACCTTATCCGTACTGTGACGACGAGATGCACTTGCCACCGCACCATCTCGCTGTGAGA	450
462	QY		CGGGGAGGAGCCCCACCCCTTACCAGGGGCCCTGCACCTTCGACTTCGGGAGCCCGGAGCA	521
451	DB		CGGGGAGGAGCCCCACCCCTTACCAGGGGCCCTGCACCTTCGACTTCGGGAGCCCGGAGCA	510
522	QY		GCAGCTGGAACCTGAACCGGGAGTCGGTGGCGGCAACCCCAACAGAAACATCTTTCGACAG	581
511	DB		GCAGCTGGAACCTGAACCGGGAGTCGGTGGCGGCAACCCCAACAGAAACATCTTTCGACAG	570
582	QY		TCGACCTGATGATAGTGTGACGGCTGGGCGGGCCCCCTGCCCCCCAGACAGATAACTCGGGGCAT	641
571	DB		TGACCTGATGATGATGTGCAGGCTGGGGGGCCCCCTGCCCCCCAGACAGATAACTCGGGGCAT	630
642	QY		CAGCGCCACGTGCTTACGGGACGGGGGGCGCATGGAGGGGCCCGCCGCACTACAGCA	701
631	DB		CAGCGCCACGTGCTTACGGGACGGGGGGCGCATGGAGGGGCCCGCCGCACTACAGCA	690
702	QY		GGTCATCGGCCCACTACCGCGGGGTCTCTCTTCCAGCACACGACAGACAGTGGGCGCGCTTC	761
691	DB		GGTCATCGGCCCACTACCGCGGGGTCTCTCTTCCAGCACACGACAGACAGTGGGCGCGCTTC	750
762	QY		CTTGTGTGAGGGGACCGCGCTTCACCACACACATCGCGCCCTTAGAGAGCGCAGCCAT	821
751	DB		CTTGTGTGAGGGGACCGCGCTTCACCACACACATCGCGCCCTTAGAGAGCGCAGCCAT	810
822	QY		CTGGACAAAGAGAAAGATAAACAGAAAGCACCCCTCTC	861
811	DB		CTTGGACTAAGAGAAAGATAAACAGAAAGCACCCCTCTC	850

```

RESULT 2
US-09-769-482-2
; Sequence 2, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-769-482-2

Query Match      87.4%; Score 752.8; DB 4; Length 759;
Best Local Similarity 99.7%; Pred. No. 9.6e-164;
Matches 754; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      106  ATCACGGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGTGGTATCATGGTATGGTG 165
Db       1  ATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTATCATGGTATGGTG 60

QY      166  GTGGTGATCACCTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCTCTTCATCAGCCGG 225

```

226	QY	CACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAAGATGCTGTGGCCCTTCG	285
121	Db		
121	Db	CACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAAGATGCTGTGGCCCTTCG	180
286	QY	GAGAGCAAGTGTTCAGGCACCGGAATCCAGAGCCGACAGTCTACGCCCCGCTTCGGCCC	345
181	Db		
181	Db	GAGAGCAAGTGTTCAGGCACCGGAATCCAGAGCCGACAGTCTACGCCCCGCTTCGGCCC	240
346	QY	ACCCAGCCGCTGGCGGTGCGCGCTTTCGCCACAGCGGAGCGCTTCCACCGCTTCAGGCC	405
241	Db		
241	Db	ACCCAGCCGCTGGCGGTGCGCGCTTTCGCCACAGCGGAGCGCTTCCACCGCTTCAGGCC	300
406	QY	ACCTATCCGTACTTCGACGACGAGATCGACCTTGCACCCACCATCTCGTGTTCAGACGG	465
301	Db		
301	Db	ACCTATCCGTACTTCGACGACGAGATCGACCTTGCACCCACCATCTCGTGTTCAGACGG	360
466	QY	GAGAGCCCCACCCCTACCAAGGCGCCCTGACACCTCCAGCTTCGGGACCCCGAGCAGCAG	525
361	Db		
361	Db	GAGAGCCCCACCCCTACCAAGGCGCCCTGACACCTCCAGCTTCGGGACCCCGAGCAGCAG	420
526	QY	CTTGAAACTGAAACCCGGGAGTCCGTGCGCGCACCCCCAAAACAGAACCATCTTCGACAGTGAC	585
421	Db		
421	Db	CTTGAAACTGAAACCCGGGAGTCCGTGCGCGCACCCCCAAAACAGAACCATCTTCGACAGTGAC	480
586	QY	CTGATGAGTATGTCACGGCTTGGCGGCGCCCTGCGCCGCCAGCAGTAACCTCGGGCATCAGC	645
481	Db		
481	Db	CTGATGAGTATGTCACGGCTTGGCGGCGCCCTGCGCCGCCAGCAGTAACCTCGGGCATCAGC	540
646	QY	GCCACGTCTACTGGCAGCGCGGCGCGCATGAGGAGGGCGCGCGCCCACTACAGCGAGTTC	705
541	Db		
541	Db	GCCACGTCTACTGGCAGCGCGGCGCGCATGAGGAGGGCGCGCGCCCACTACAGCGAGTTC	600
706	QY	ATCGGCCCATACCGGGGTCTCTTCTTCAGCAACGAGCAGCAGTGGCGCGCCCTCTCTTG	765
601	Db		
601	Db	ATCGGCCCATACCGGGGTCTCTTCTTCAGCAACGAGCAGCAGTGGCGCGCCCTCTCTTG	660
766	QY	CTGGAGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCATCTCG	825
661	Db		
661	Db	CTGGAGGGGACCCGGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCATCTCG	720
826	QY	AGCAAGAGGAAGGATAAACAAGAAAGGACACCTCTC	861
721	Db		
721	Db	AGCAAGAGGAAGGATAAACAAGAAAGGACACCTCTC	756

RESULT 3
US-09-091-952A-7
; Sequence 7, Application US/09091952A
; Patent No. 6458532
; GENERAL INVENTION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Escerling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7

Query Match 40.9%; Score 352.2; DB 3; Length 921;

Best Local Similarity 73.1%; Pred. No. 1.2e-71;

Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY	94	CAGAGCATGAGATCAGCGAGCTGGAGTTTTCAGATCATCATCATCGTGGTGGTATG	153
DB	166	CGGGCTCTTCACTCGAGCTGGAGTTTCGCCAAATCATCATCATCGTGGTGGTC	225
QY	154	ATGTTGATGTTGGTGGTATCAGTCTGCTGAGCCACTACAGCTGTGACCGTCC	213
DB	226	ACGGTATGTTGGTGGTATCATGCTGCTGCTGAACCACTACAAATCTCACCGGTCC	285
QY	214	TTATCATCGCGGCACACCGAGCGCGGAGGAGAGATGCCCTGTCTCAGAGGATGC	273
DB	286	TTATCAACCGCCCGAACAGCGCGGAGCGGGCTGCCAGGAGGAGGTGC	345
QY	274	CTGTGGCCCTCGGAGAGCAGTGTCTAGGCAACGGAAATCCAGAGCGCGAGTCTAGCC	333
DB	346	CTGTGGCTTTCAGACAGCGCGCACCGCGGTGG-----CGCTCGAGATCATGCAT	399
QY	334	CGCTCGCGCCACCGACCGCTGGCGCTGCCCGCTTCCCGCGGAGCGCTTCCAC	393
DB	400	GCCTCGCGGTTCAGGAGACAGTTTACAGCGCGCTTCTTCAGAGGATCGCTTCAGC	459
QY	394	CGCTTCAGCGCCACTATCGTACTCTCAGCAGCAGATCGACTGCCACCCACCATCTCG	453
DB	460	CGTTTCAGCGCCACTTACCTCTATGTGAGCAGCAGAGATTGATCTTCTCCCACTCC	519
QY	454	CTGTTCAGCGGGAGGAGCGCCCAACCTTACAGGGCCCTTGCACCTTCAGCTTGGGAC	513
DB	520	CTGTCCGAGCGTGAAGAGCGACCTCTTACAGGGGCGCTTGCACCTTGCAGCTCCGGAC	579
QY	514	CCCGAGCGAGCTGGAACTGAACCGGAGTCTGGTGGCGCACCCCAACAGACCATC	573
DB	580	CCTGAACAGAGATGGAACTCAACCGAGATCGTGTAGGCGCCCAACCAACCGAACA	639
QY	574	TTGACAGTACCTGATGGATAGTGGCAGG---CTGGGCGCGCCCTGCCCCCCAGCAGT	630
DB	640	TTTGACAGTGAATTAATAGACTTCTATGTATAGCGGGGTCTCATGCCCAACCGAGC	699
QY	631	AACTCGGGCATCAGCGCCAGCTGTCTACGGAGCGCGGCGCATGGAGGGCGCGCGCC	690

DB	700	AACTCGGGCATCAGTCAAGCACCTGCAGCAGTAAACGGAGGATGGAGGGGCCACCCCC	759
QY	691	ACCTACAGCGAGGTCTATCGGCCACTACCCGGGGTCTCTTCCAGCACCAGCAGCAG	749
DB	760	ACATACAGCGAGGTGATGGCCACCACCCAGGCGCTCTTCTCTCCATCACCAGCGCAG	818

RESULT 4
US-09-091-952A-6
Sequence 6, Application US/09091952A
Patent No. 6458532
GENERAL INFORMATION:
APPLICANT: Detera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1...8065
OTHER INFORMATION: Clone 22
FEATURE:
NAME/KEY: CDS
LOCATION: 116...1036
OTHER INFORMATION: Clone 22 coding region
FEATURE:
NAME/KEY: misc feature
LOCATION: 452...505
OTHER INFORMATION: alternatively spliced portion


```
; NAME/KEY: misc feature
; LOCATION: 5595...5685
; OTHER INFORMATION: amplified region for genotyping
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-091-952A-6

Query Match      40.9%; Score 352.2; DB 3; Length 8065;
Best Local Similarity 73.1%; Pred. No. 2.2e-71;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 94 CAGAGCATGGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTATG 153
Db 281 CCGGCGATCTTCAACTCGGAGCTGGAGTTGCCCAAAATCATCATCTCGTGGTGGTGC 340
QY 154 ATGTGTATGGTGGTGGTATCATCGCTGCTGAGCCACTACAGAGTGTCTGACAGGTCC 213
Db 341 ACGGTATGGTGGTGGTATCGTCTGCTGTGACCACTACAAAGTCTCAACGCGGTCC 400
QY 214 TTCTATCGCCGGCACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGC 273
Db 401 TTCTATCAACCCCGCAACAGAGCCGAGGCGGAGGACGGGCTGCCGAGGAAGGTTGC 460
QY 274 CTGTGGCCCTCGGAGAGCAGAGTGTACAGCAACGGAATCCAGAGCCGAGGTCTAGCC 333
Db 461 CTGTGGCCCTTCAGACAGCGCCGACACCGCGGTGGG-----CGCTCGGAGATCATGCAT 514
QY 334 CCGCTCGGCCCAACCGAGCCGCTGGCGGTGCGGCCCTTCGCCCAAGCGGAGCGCTTCCAC 393
Db 515 GCCCGCGGTCCAGGAGACAGTTTCACAGCGCGGTCTTCATCAGAGGATCGCTTCAGC 574
QY 394 CGCTTCAGCCCACTATCGTACCTGAGCAGCAGAGATGCACTGCAACCCACCATCTCG 453
Db 575 CGCTTCAGCCCACTATCGTACCTGAGCAGCAGAGATGCACTGCAACCCACCATCTCC 634
QY 454 CTGTTCAGACGGGAGGAGCCCAACCTTACAGGGCCCTGCAACCTTCAGCTTCGGGAC 513
Db 635 CTGTTCAGACGGTGAAGAGCACACTTCCTTACAGGGGCCCTGCAACCTTCAGCTTCGGGAC 694
QY 514 CCGAGCAGCAGCTGGAACCTGAACCGGGAGTCCGTGCGGCCCAACCCCAACAGAACCATC 573
Db 695 CCTGAACAGCAGATGGAACCTGAACCGAGATCCGTGAGGGCCCAACCCCAACAGAACCATC 754
QY 754 TTGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 630
Db 755 TTTGACAGTATTTAATAGACATTTGATGATGATGATGATGATGATGATGATGATGATGATG 814
QY 631 AACTCGGGCATCAGCGCCACGTGTACGGCAGCGGGGGCGCATGGAGGGGGCGCGCC 690
Db 815 AACTCGGGCATCAGTGAACACCTGACAGCATGTAACGGGAGGATGAGGGGGCCACCC 874
QY 691 ACCTACGAGGATCATCGGCCACTACCCGGGTCTCTCTTCAGCAGCAGCAGAGCAG 749
Db 875 ACATACGAGGATGATGGGCCACCCAGCGGCGCTCTTCTCTCATCAGCAGCGCAG 933

RESULT 5
US-09-311-021-65
; Sequence 65, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311, 021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 937

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-311-021-65

Query Match      40.8%; Score 351.6; DB 4; Length 937;
Best Local Similarity 73.0%; Pred. No. 1.7e-71;
Matches 482; Conservative 0; Mismatches 169; Indels 9; Gaps 2;

QY 93 CAGAGCATGGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTAT 152
Db 134 CTTGTCTTTAAAAAAGCGAGCTGGAGTTGCCCAAAATCATCATCTCGTGGTGGTAT 193
QY 153 GATGTGTATGGTGGTGGTATCATCGCTGCTGAGCCACTCAAGCTCTCTGACGGTCC 212
Db 194 CAGGTGTATGGTGGTGGTATCATCTGCTGTGAAACCACTACAAAGTCTTCACCGGGTCC 253
QY 213 CTTTCATCAGCCGGCACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCAGAAAGGATG 272
Db 254 CTTTCATCAACCGCCGCAACAGAGCCGAGGCGGAGGACGGGCTGCCCGCAGGAAGGGTGC 313
QY 273 CTTGTGGCCCTCGGAGAGCAGAGTGTACAGCAACGGAATCCAGAGCCGAGGTCTACGC 332
Db 314 CTTGTGGCCCTTCAGACAGCGCCGACCGCGCTGGGG-----CGCTCGGAGATCATGCA 367
QY 333 CCGCTCGGCCCAACCGAGCCGCTGGCGGTGCGGCCCTTCGCCCAAGCGGAGCGTTCCTCA 392
Db 368 TGCCCGCGGTTCAGGAGCAGAGTTTACAGCGCGGTCTTCATCAGAGGATCGCTTCAG 427
QY 393 CGCTTCAGCCCACTATCGTACCTGAGCAGCAGAGATGCACTGCAACCCACCATCTCTC 452
Db 428 CGCTTCAGCCCACTATCGTACCTGAGCAGCAGAGATGCACTTCTCTCCACCATCTCTC 487
QY 453 GTGTTCAGACGGGAGGAGCCCAACCTTACAGGGCCCTGCAACCTTCAGCTTCGGGA 512
Db 488 CTGTTCAGACGGTGAAGAGCACACTTCCTTACAGGGGCCCTGCAACCTTCAGCTTCGGGA 547
QY 513 CCGCAGCAGCAGCTGGAACCTGAACCGGGAGTCCGTGCGGCCCAACCCCAACAGAACCATC 572
Db 548 CCTGAACAGCAGATGGAACCTGAACCGAGATCCGTGAGGGGCCCAACCCCAACAGAACCAT 607
QY 573 CTTTCAGAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 629
Db 608 ATTGACAGTGAATTAATAGACATTTGATGATGATGATGATGATGATGATGATGATGATGATG 667
QY 630 TAACTCGGGCATCAGCGCCACGTGTACGGCAGCGGGGGCGCATGGAGGGGGCGCGCC 689
Db 668 CAACTCGGGCATCAGTGAACACCTGACAGCATTAACGGGAGGATGAGGGGGCCACCC 727
QY 690 CACTACAGCGAGGTATCTGCGCCACTACCCGGGTCTCTCTTCAGCAGCAGCAGAGCAG 749
Db 728 CACATACAGGAGTGTATGGGCCACCCAGCGGCGCTCTTCTCTCATCAGCAGCGCAG 787

RESULT 6
US-09-091-952A-8
; Sequence 8, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic
; Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```


STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASCSQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..867
OTHER INFORMATION: Clone 22 isoform 2 alternatively
spliced coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-091-952A-8

Query Match 33.0%; Score 284.2; DB 3; Length 867;
Best Local Similarity 68.7%; Pred. No. 5e-56;
Matches 453; Conservative 0; Mismatches 143; Indels 63; Gaps 2;
QY 94 CAGAGATGGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCATCTGCTGGTGGTATG 153
DB 166 CCGGCACTTCAACTCGGAGCTGGAGTTGCCCAATCATCATCTGCTGGTGGTGC 225
QY 154 ATGTTAGTGTGGTGTGATCAGTCTGCTGAGCCACTACAGCTGTCTGCAAGTCC 213
DB 226 ACGTGTATGTTGGTGTGTCATCTGCTGCTGAACCACTACAAAGTCTCCACGCGTCC 285
QY 214 TTCTATGAGCGGCACACCGAGGCGGAGGAGAGAGATGCCCTGTCTCAGAGGATGC 273
DB 286 TTCTATCAACCGCCCGAACCAAGAGCGGAGCGGAGGAGCGGCT----- 329
QY 274 CTGTGGCCCTCGGAGAGCAGATGTCTAGGCAACGGAATCCAGAGCGGAGGTTCTAGCC 333
DB 330 -----GCCGAGATCATGTCAT 345
QY 334 CCGCTCTGGCCCAACCGACCGCTGGCGTGGCCCTTCCGCCAGCGGAGCGCTTCCAC 393
DB 346 GCCCGCGGTCCAGGGACAGGTTTCACAGCGCGTCTTCATCCAGAGGATGCTTCAGC 405
QY 394 CGCTTCAGCGCCACTATCGTACCTGTCAGACAGATGACCTGCCACCCACCATCTCG 453
DB 406 CGCTTCAGCGCCACTATCGTACCTGTCAGACAGATGATCTCTCCACCATCTCC 465
QY 454 CTGTTCAGCGGGAGGAGCCCAACCTTACAGGGCCCTTGCACCTCCAGCTTCGGGAC 513
DB 466 CTGTTCAGCGGGTGAAGAGCACCTCTCTTACAGGGCCCTTGCACCTTCGAGCTCCGGAC 525
QY 514 CCGAGCAGCAGCTGGAACTGAACCGGGAGTCTGGTGGCGCACCCGCCCAACAGAACCATC 573

DB 526 CCTGAACAGCAGATGGAACTCAACCGAGAGTTCGTGAGGGGCCCCACCAACCCGAACATA 585
QY 574 TTGACAGTGCACCTGATGGATAGTGCCAGG---CTGGGCGGCGCCCTGCCCCCCCCCAGCAGT 630
DB 586 TTTGACAGTGAATTAATAGACATTTGCTATGTATAGCGGGGTCCATGCCCCCAGCAGCAGC 645
QY 631 AACTCGGGCATCAGCGCCACGTCGTACGGCAGCGGGCGGCGCATGGAGGGGCGCGCCCC 690
DB 646 AACTCGGGCATCAGTGCAGACGCTGCAAGCACTGCGAGCAGTAAACGGGAGGATGGAGGGGCCACCCCCC 705
QY 691 ACCTACAGCGAGTTCATCGGCCCACTACCGGGGTCTCTTCCAGACACGAGCAGCAG 749
DB 706 ACATACAGCGAGTGTGAGGGCCACCCAGCGGCGCTCTTTCTCTCATCATCCAGCGCAG 764
RESULT 7
US-09-621-976-2162
; Sequence 2162, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2162
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 17..223
US-09-621-976-2162

Query Match 10.5%; Score 90.4; DB 4; Length 391;
Best Local Similarity 75.7%; Pred. No. 1.4e-11;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 607 GGGCGGCGCTGCGCCCGCCAGCAGTAATCTCGGGCATCAGCGCCACGCTGCTACGGCAGCGC 666
DB 26 GGGGGTCCATGCCACCCAGCAGCAACTCGGGCATCAGTCCAGCACCTTCAGCAGTAAC 85
QY 667 GGGCGCATGAGGGGGCGCGCCCACTACAGCAGGTCTATCGGCCACTACCGGGGTCC 726
DB 86 GGGAGGATGGAGGGGGCCACCCCCACATACAGCGAGGTGATGGGCCACCCAGCGCGCC 145
QY 727 TCCTTCCAGCAGCAGCAGCAGTGGGC 754
DB 146 TCTTCTCTCATCACCAGCGCAGAACGC 173

RESULT 8
US-09-902-540-6620
; Sequence 6620, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6620


```

; LENGTH: 645
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6620

      Query Match          6.6%; Score 57.2; DB 4; Length 645;
      Best Local Similarity 45.7%; Pred. No. 0.00069;
      Matches 200; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 296 TGT CAGGCAACGGAAATCCAGAGCGCAGGTCTACGCCCGCCCTCGGCCACCGACCGCC 355
Db 80 TGGCGGACGGCGCATCTCTGAAAGTGGTGAGGAGAACCCCTTCTCTGTCCAGCTTCTACA 139
QY 356 TGGCGGTGCCCGCTTCGCCCAGCGGGAGCGCTTCCACCGTTCAGGCCACCTATCCGT 415
Db 140 CGAACCGGCAAGATTCCGTTCCAGAGCGAGATCTTCTTCTCTGTGCGGCTTCGGTC 199
QY 416 ACCTGCAGCAGAGATCGACCTGCCACCCACCATCTCGCTGTACAGCGGAGAGAGCCCC 475
Db 200 AGCAGCAGGAGCTGTTCACGAGGACCTTTCAGCTCGATGACGGTCAGCGACTACTGT 259
QY 476 CACCTTACCAGGGCCCTGCACTCTCAGCTTGGGAGCCCGAGCAGCAGCTGGAATGA 535
Db 260 TCGCAAGGACCGCATCTTCGCGACCTCAACTGGACGGCAGAGCTGGCCCTCTACG 319
QY 536 ACCGGGAGTCGGTGGCGGCACCCCCAAACAGAACCATCTTCGACAGTGACTGATGATA 595
Db 320 AGCGGTCTTCAGAGCGCTGGGGCCCGGTGGCCAGCGGAACTGGTCACTCACTCC 379
QY 596 GTGCCAGCTGGGGCGGCCCTTGCCCCCGCAGCAGTAATCTGGGCATCAGGCCACGTGCT 655
Db 380 AGGCCCGACTGGACGTGCTCTGTCACCGCATCAAGAGCGCGCGGAGTTCGAGCGCA 439
QY 656 ACGGCACGGCGGCGCATGAGGGCGCGGCCACCTACAGGAGGTCACTCGGCCACT 715
Db 440 AGTTGACCCCACTGACTGAGGGGCTCGTCCACTCTCAACAACACTTCTTCTCCACT 499
QY 716 ACCGGGGTCTCTCTCC 733
Db 500 ACAGGACACCCCGCTCC 517

RESULT 9
US-09-902-540-506
; Sequence 506, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 506
; LENGTH: 2364
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-506

      Query Match          6.6%; Score 57.2; DB 4; Length 2364;
      Best Local Similarity 45.7%; Pred. No. 0.00098;
      Matches 200; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 296 TGT CAGGCAACGGAAATCCAGAGCGCAGGTCTACGCCCGCCCTCGGCCACCGACCGCC 355
Db 734 TGGCGGACGGCGCATCTCTGAAAGTGGTGAGGAGAACCCCTTCTCTGTCCAGCTTCTACA 793
QY 356 TGGCGGTGCCCGCTTCGCCCAGCGGGAGCGCTTCCACCGTTCAGGCCACCTATCCGT 415

```


Qy	531	ACTGAA	CGGGAGT	CGGTG	CGCGG	CACCC	CAAA	CAGAA	CCAT	CTT	CGAC	AGT	GAC	CTGAT	590
Db	1216	A--GA	CGGCAC	GAGAA	GTGCC	CCAC	GGCG	CAGCA	CCAC	CGCC	ACCG	CGG	AGCC	AGCC	1273
Qy	591	GGATAG	TGCCAGG	TGCGG	CGGCC	CCCT	TGCCCC	CCCC	CAGCA	GAT	AACT	CTCG	GGCAT	CAGCG	650
Db	1274	GTGAGG	CGCGG	CGGT	ATAC	CGT	CACT	CTCT	CGGA	AGCG	ACAT	CCAT	TAT	CAG	1333
Qy	651	GTGCTA	CGC	AGCGG	CGCG	ATG	AGGGG	CCCG	CGCC	CACT	TA	CAG	CGAG	GT	710
Db	1334	GAGCTG	CGAGA	AGGCG	CGCT	TA	CGGCC	CA	CAGG	CAG	ACGA	AGG	CGG	CAG	1393
Qy	711	CCA	CTACC	CGGGG	CTCT	CTCT	TCC	AGC	ACC	CAG	CAG	CAG	TGGG	CGCC	770
Db	1394	CGGAGG	AGT	GTGCG	CGGT	CCCA	TCAT	CAG	CGCG	CGAA	CTGT	CCCC	CGG	CGCC	1453
Qy	771	GGG	GAC	776											
Db	1454	CGC	GAC	1459											

RESULT 11

US-09-902-540-8567/c

; Sequence 8567, Application US/09902540

; Patent NO. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 8567

; LENGTH: 1884

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-8567

Db	1452	GAGCAGCAGGGTCCCCAGCCCGGAGGAACTGCGCCGGTCCCATCAACGGCCGAACTGTCC	1393
Qy	753	GCGCCCTCTTGTCTGGAGGGGAC	776
Db	1392	CGCGCCCGCGCGCGTGGCGCGAC	1369

RESULT 12

US-09-949-016-3915

; Sequence 3915, Application US/09949016

; Patent NO. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3915

; LENGTH: 1122

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-3915

Query Match	6.1%;	Score 52.6;	DB 4;	Length 1884;
Best Local Similarity	48.0%;	Pred. No. 0.011;		
Matches 213;	Conservative 0;	Mismatches 256;	Indels 5;	Gaps 2;
Qy	336	GCTTCGGCGCCACCGACCGCTTGGCCGTGGCGCCCTTTCGCCACGGGAGCGCTTTCACCG	395	
Db	1810	GCAGCCACACGCGGCCACCGTCCAGCCCCCAACGCGCGGCCACCGCGTGACGCTGGTCC	1751	
Qy	396	CTTCCAGCCCACTATCGGTACTGTGCAGCAGCAGATCGACTGCCACCCACCATCTCGCT	455	
Db	1750	AGTGGAAACGACCGCTGCCGGATGAAGCGCGGGAACACACAGCAGTAGACGTCACGC	1691	
Qy	456	GTGACGCGGGAGGAGCCCCACCTACCAGGGCCCTGCAC---	512	CCTCAGCTTCGGGA
Db	1690	CCCGCATCAGGAGCAGGCCACGCCCCACGACGCGGAGTGCCTTGGGTCTCTGCTTCAGGC	1631	
Qy	513	CCCGAGCAGCAGCTGGACGTGACCGGAGTCGGTGGCGGCACCCCCACACAGAACCAT	572	
Db	1630	GCGGAGGAGCAGCAGGAA--GAACGGCAGCAAGTGGCCCCACGCCACAGCACCCGC	1573	
Qy	573	CTTCGACAGTGACCTGATGGATAGTGCCAGCGCGGGCGCCCTGCCCCCAGCAGCTAA	632	
Db	1572	CACCGAGCCGACCAACCGTCGAGCGCGCGCGGTACAAGTCACTCTCTCCGGAAGCGA	1513	
Qy	633	CTCGGGCATCAGCGCCACGTCTACGGCAGCGCGCGCGCATGAGAGGGCGCGCCGCCAC	692	
Db	1512	CGCAATCATATCAGCAGGAGCTCGGAGAGGCCCGGTACGCCCAAGGCAGACGAAGGC	1453	
Qy	693	CTACAGCGAGGTCAATCGGCCACTACCGGGGTCTCTCTTCAGCACACAGCAGACGACGTGG	752	

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13687
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13687

Query Match 5.6%; Score 48; DB 4; Length 696;
Best Local Similarity 57.2%; Pred. No. 0.092;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACCGAGCTGGAGTTGTTTCAGATCATCATCTGTTGGTGTGATGATGTTGGTGTG 168
DB 482 ACCCTGCTGAATTCCTGTTCCGATCTGTCGCGCGGGTGGTCTCTGGCGGTGGTCTG 541

QY 169 GTGATCAGTCCCTGCTGAGCCTACAGCTGTCTGACCGTCTCTTCATCAGCCGGCAC 228
DB 542 CTGGTCAAGCGCCTGCTGCTCGAAGAGAAAGAACTGGCTGAGCCTGCCATCGCCGGCAG 601

QY 229 AGCCAGGGCGGAGAGAGAGATGCCCTGTC 260
DB 602 CGCCATCGGAGGGCGGATAGCCGCCCTGGC 633

RESULT 14
US-09-252-991A-13650/c
; Sequence 13650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13650
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13650

Query Match 5.6%; Score 48; DB 4; Length 1452;
Best Local Similarity 57.2%; Pred. No. 0.11;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACCGAGCTGGAGTTGTTTCAGATCATCATCTGTTGGTGTGATGATGTTGGTGTG 168
DB 267 ACCCTGCTGAATTCCTGTTCCGATCTGTCGCGCGGGTGGTCTCTGGCGGTGGTCTG 208

QY 169 GTGATCAGTCCCTGCTGAGCCCTACAGCTGTCTGCAAGGTCCTTCATCAGCCGGCAC 228
DB 207 CTGGTCAAGCGCCTGCTGCTCGAAGAGAAAGAACTGGCTGAGCCTGCCATCGCCGGCAG 148

QY 229 AGCCAGGGCGGAGGAGAGATGCCCTGTC 260
DB 147 CGCCATCGGAGGGCGGATAGCCGCCCTGGC 116

RESULT 15
US-09-949-016-15657

; Sequence 15657, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15657
; LENGTH: 8154
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15657

Query Match 5.6%; Score 47.8; DB 4; Length 8154;
Best Local Similarity 47.4%; Pred. No. 0.2;
Matches 176; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

QY 323 AGTCTACGCCCGCTCGGCCACCGACCGCTGTCGCGCTGCGCCCTTCGCCCGAGCGGG 382
DB 2306 AGTTGCCCTGTGCCCGGGGAGCCCGCGGCTGGCCAAAGTACGGGCTGC 2365

QY 383 AGCGCTTCCACCGCTTCCAGCCCACTATCCGTACTCTGACGACGAGATCGACCTGCCAC 442
DB 2366 CGGGCTGGCGAGCTCAAGAGCCCGAGTCTGATGCTGTGCTA---CGACCCGCGCA 2422

QY 443 CCACCATCTCGTGTGTCAGACGGGGAGGAGCCGCCCTTACCAGGGGCGCCCTGCACCTCC 502
DB 2423 CCGCGCGCGCTCTGGGTGGTGGAGAGCTGCGACCCGAGCGTCTCCGCGCGAGCGGG 2482

QY 503 AGCTTGGGACCCCGAGCAGAGCTGGAACTGACCGGGAGTGGTGGCGGACCCCA 562
DB 2483 ACCGCGGAGTGGCGACTTCCGCGAGGACGACTCGGTGACGCGTACCACCGTGCACCA 2542

QY 563 ACAGAACCATCTTCGACAGTACCTGATGGATAGTGCAGGCTGGGCGGCGCCCTGCCCC 622
DB 2543 AGCGGACTTACCGCGGAGTGGCTTCGACCGCGGTCACTGGCGCGCGCCGCGCAACCA 2602

QY 623 CCAGCAGTAATCTCGGGCATCAGCGCCACGTCCTACGGCAGCGGGCGGCGCATGGAGGG 682
DB 2603 GCTGAGGCGAAGGCGCATGGACGACACAGTCTTACCTGAGCAACGTCGCGCGCCAGGTAG 2662

QY 683 CGCGCGCCACCC 693
DB 2663 CGCGCGCGCC 2673

Search completed: February 19, 2005, 16:22:53
Job time : 161.626 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 14:21:20 ; Search time 483.77 Seconds
(without alignments)
10519.334 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcacgcgttgatgggggt.....aacagaaaggacacccctctc 861

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	861	100.0	861	9	US-09-934-249-3
2	861	100.0	864	17	US-10-295-027-127
3	861	100.0	1321	9	US-09-934-249-1
4	861	100.0	4839	15	US-10-241-220-119
5	861	100.0	4839	16	US-10-269-909-84
6	861	100.0	4839	16	US-10-269-909-85
7	861	100.0	4839	18	US-10-872-972-119
8	861	100.0	4839	18	US-10-872-991-119
9	755.2	87.7	969	10	US-09-796-753-55
10	754.2	87.6	1141	15	US-10-205-823-412
11	754.2	87.6	1141	15	US-10-301-822-208

12	754.2	87.6	1850	15	US-10-241-220-44	Sequence 44, Appl
13	754.2	87.6	1850	18	US-10-872-972-44	Sequence 44, Appl
14	754.2	87.6	1850	18	US-10-872-991-44	Sequence 44, Appl
15	754.2	87.6	4527	10	US-09-821-812-2	Sequence 2, Appl
16	754.2	87.6	4527	18	US-10-849-635-2	Sequence 2, Appl
17	753.6	87.5	1140	16	US-10-390-045-1	Sequence 1, Appl
18	753.6	87.5	1140	17	US-10-434-479-1	Sequence 1, Appl
19	752.8	87.4	759	16	US-10-390-045-2	Sequence 2, Appl
20	752.8	87.4	759	17	US-10-434-479-2	Sequence 2, Appl
21	752.6	87.4	806	15	US-10-241-220-45	Sequence 45, Appl
22	752.6	87.4	806	18	US-10-872-972-45	Sequence 45, Appl
23	752.6	87.4	806	18	US-10-872-991-45	Sequence 45, Appl
24	742.4	86.2	1066	13	US-10-098-841-71	Sequence 71, Appl
25	612.4	71.1	878	9	US-09-934-249-12	Sequence 12, Appl
26	544.4	63.2	1583	14	US-10-000-256A-32	Sequence 32, Appl
27	462.2	53.7	1713	10	US-09-796-753-57	Sequence 57, Appl
28	445.6	51.8	693	9	US-09-934-249-14	Sequence 14, Appl
29	352.2	40.9	921	16	US-10-251-598-7	Sequence 0, Appl
30	352.2	40.9	8018	13	US-10-087-192-1667	Sequence 1667, Ap
31	352.2	40.9	8065	16	US-10-251-598-6	Sequence 0, Appl
32	350	40.7	920	9	US-09-823-245A-20	Sequence 20, Appl
33	350	40.7	2170	17	US-10-094-749-197	Sequence 197, App
34	349	40.5	8093	9	US-09-934-249-16	Sequence 16, Appl
35	349	40.5	8093	17	US-10-172-118-1023	Sequence 1023, Ap
36	349	40.5	8093	17	US-10-342-887-1023	Sequence 1023, Ap
37	341.8	39.7	475	9	US-09-934-249-15	Sequence 15, Appl
38	284.2	33.0	867	16	US-10-251-598-8	Sequence 0, Appl
39	250.2	29.1	285020	13	US-10-087-192-1666	Sequence 1666, Ap
40	134	15.6	368	9	US-09-783-590-3464	Sequence 3464, Ap
41	134	15.6	467	10	US-09-918-995-2074	Sequence 2074, Ap
42	59.2	6.9	65	9	US-09-783-590-3488	Sequence 3488, Ap
43	57	6.6	584	18	US-10-767-701-4186	Sequence 4186, Ap
44	55.4	6.4	522	17	US-10-240-425-156	Sequence 156, App
45	54.6	6.3	3133	15	US-10-017-161-1483	Sequence 1483, Ap

ALIGNMENTS

RESULT 1

US-09-934-249-3
; Sequence 3, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John P.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934,249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(861)
US-09-934-249-3

Query Match 100.0%; Score 861; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 9.6e-220;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACGCTTGATGGGGTCAACAGCCGCCGCCGCCGCCCGGCGGCGCAATGTC 60


```

; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 55
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(761)
; US-09-796-753--55

Query Match      87.7%; Score 755.2; DB 10; Length 969;
Best Local Similarity 99.6%; Pred. No. 1.6e-191;
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 102 GGAGATCAGGAGTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTGGTAT 161
Db 2 GGAGATGGCGGAGTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTGGTAT 61

QY 162 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 221
Db 62 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121

222 CCGGCAAGCCAGCGGCGGAGGAGAGAAAGATGCGCTGTCTCTCAGAAAGATGCTGTGGCC 281
122 CCGGCAAGCCAGCGGCGGAGGAGAGAAAGATGCGCTGTCTCTCAGAAAGATGCTGTGGCC 181
282 CTCGGAGAGCACAGTGTCTAGGCAACGGAATCCAGAGCCGCGAGTCTTACGCCCCGCTCG 341
182 CTCGGAGAGCACAGTGTCTAGGCAACGGAATCCAGAGCCGCGAGTCTTACGCCCCGCTCG 241
342 GCCCACCAGCCGCTGGCCCTGCGCCCTTTCGCCCCAGCGGGAGCGCTTCCACCGCTTCCA 401
242 GCCCACCAGCCGCTGGCCCTGCGCCCTTTCGCCCCAGCGGGAGCGCTTCCACCGCTTCCA 301
402 GCCCACCATCTATCTGTACCTGTCAGCAACGAGATCGACTGCGCAACCACTCTCGTGTGAGA 461
302 GCCCACCATCTATCTGTACCTGTCAGCAACGAGATCGACTGCGCAACCACTCTCGTGTGAGA 361
462 CGGGGAGGAGCCGCCACCTTACCAGGGCCCTTCCAGCCCTCCAGCTTCCGAGCCCGGAGCA 521
362 CGGGGAGGAGCCGCCACCTTACCAGGGCCCTTCCAGCCCTCCAGCTTCCGAGCCCGGAGCA 421
522 GCAGCTGGAACTGAACCGGGAGTGGTGGCGCGCACCCCAAAACAGAACCACTTTCGACAG 581
422 GCAGCTGGAACTGAACCGGGAGTGGTGGCGCGCACCCCAAAACAGAACCACTTTCGACAG 481
582 TGACCTGATGGATAGTGCAGGCTGGGGCGGCCCTTCCAGCAACCACTTTCGAGCAAT 641
482 TGACCTGATGGATAGTGCAGGCTGGGGCGGCCCTTCCAGCAACCACTTTCGAGCAAT 541
642 CAGCGCCAGTGTCTACGGCAGCGGGCGGCGCATGGAGGGGCGCGCCGCCCTTACAGCGA 701
542 CAGCGCCAGTGTCTACGGCAGCGGGCGGCGCATGGAGGGGCGCGCCGCCCTTACAGCGA 601
702 GGTCTATCGGCCACTTACCGGGGTCCTCTTCCAGCAGCAGCAGCAGCAGTGGGGCGGCTC 761
602 GGTCTATCGGCCACTTACCGGGGTCCTCTTCCAGCAGCAGCAGCAGCAGTGGGGCGGCTC 661
762 CTTGCTGGAGGGGAGCCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGGCGCAT 821
662 CTTGCTGGAGGGGAGCCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGGCGCAT 721
822 CTGGAGCAAGAGAGAGGATTAACAGAAAGGACACCCCTCTC 861
722 CTGGAGCAAGAGAGAGGATTAACAGAAAGGACACCCCTCTC 761

RESULT 10
US-10-205-823-412
; Sequence 412, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wensey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
```



```
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 60/341,746
/ PRIOR FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: 60/362,158
/ PRIOR FILING DATE: 2002-03-05
/ NUMBER OF SEQ ID NOS: 455
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 412
/ LENGTH: 1141
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-205-823-412

Query Match      87.6%; Score 754.2; DB 15; Length 1141;
Best Local Similarity 98.3%; Pred. No. 3.1e-191;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGT 146
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 147 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 206
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 137 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 196
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 207 ACGTCTTTCATCAGCCGCGCACAGCCAGGGGGGAGGAGAGAGATGCTTCTCTCAGA 266
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 197 ACGTCTTTCATCAGCCGCGCACAGCCAGGGGGGAGGAGAGATGCTTCTCTCAGA 256
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 267 AGGATGCTTGGCCCTCGGAGAGACAGTGTCTAGGCAACGGAATCCAGAGCCGAGGT 326
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 257 AGGATGCTTGGCCCTCGGAGAGACAGTGTCTAGGCAACGGAATCCAGAGCCGAGGT 316
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 327 CTAGCCCGGCTCGGCCACCGACCGCTGGCGGTGGCGGCTTCCGCCAGCGGAGCG 386
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 317 CTAGCCCGGCTCGGCCACCGACCGCTGGCGGTGGCGGCTTCCGCCAGCGGAGCG 376
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 387 CTTCACCGCTTCAGAGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 446
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 377 CTTCACCGCTTCAGAGCCACCTATCCGTACCTGACGACGAGATCGACCTGCCACCCAC 436
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 447 CATCTCGTGTTCAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 506
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 437 CATCTCGTGTTCAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 496
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 507 TCGGGAGCCCGAGCAGCTGGAACTGAACCGGGAGTGGTGGCGGAGCAGGAGGAGGAGGAG 566
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 497 TCGGGAGCCCGAGCAGCTGGAACTGAACCGGGAGTGGTGGCGGAGTGGTGGCGGAGCAG 556
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 567 AACCATCTTCGACAGTGAACCTGATGATAGTGCAGGCTGGGCGGCGGCGGCGGCGGCGG 626
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 557 AACCATCTTCGACAGTGAACCTGATGATAGTGCAGGCTGGGCGGCGGCGGCGGCGGCGG 616
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 627 CAGTAACTCGGGCATCAGCCGACGCTGCTACGGCAGCGCGGCGGCGGCGGCGGCGGCGG 686
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 617 CAGTAACTCGGGCATCAGCCGACGCTGCTACGGCAGCGCGGCGGCGGCGGCGGCGGCGG 676
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 687 GCCCACTTACAGCAGGTCTATCGGCCATACCCGGGGTCTCTTTCAGACACAGCAGAG 746
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 677 GCCCACTTACAGCAGGTCTATCGGCCATACCCGGGGTCTCTTTCAGACACAGCAGAG 736
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 747 CAGTGGGCGGCGGCTCTCTTGTGGAGGGGACCGGGCTCCACACACACATCGCGGCGCT 806
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 737 CAGTGGGCGGCGGCTCTCTTGTGGAGGGGACCGGGCTCCACACACATCGCGGCGCT 796
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 807 AGAGAGCGAGCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCTCTC 861
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 797 AGAGAGCGAGCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCTCTC 851
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-301-822-208
/ Sequence 208, Application US/10301822
```


QY 627 CAGTAACTCGGGGATCAGCGCCACGCTGCTAGCGCAGCGGGGGGCGATGAGGGGCGGCC 686
DB 617 CAGTAACTCGGGGATCAGCGCCACGCTGCTAGCGCAGCGGGGGGCGATGAGGGGCGGCC 676
QY 687 GCCCACCCTACAGGAGGTCATCGGCCCACTACCGGGGGTCTCTCTCCAGCACCAGCAGAG 746
DB 677 GCCCACCCTACAGGAGGTCATCGGCCCACTACCGGGGGTCTCTCTCCAGCACCAGCAGAG 736
QY 747 CAGTGGGCGCCCTCTCTGCTGAGGGGACCGGGTCCACCAACACACATCGCGCCCT 806
DB 737 CAGTGGGCGCCCTCTCTGCTGAGGGGACCGGGTCCACCAACACACATCGCGCCCT 796
QY 807 AGAGGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 861
DB 797 AGAGGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 851

RESULT 12
US-10-241-220-44
; Sequence 44, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-44

Query Match 87.6%; Score 754.2; DB 15; Length 1850;
Best Local Similarity 98.3%; Pred. No. 3.3e-191;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTGTGTTCCAGAGCATCGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTGTTGT 146
DB 77 TCTCCTCGGAACAGGCAATGGGAGCTGGAGTTGTTTCAGATCATCATCTGTTGT 136
QY 147 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 206
DB 137 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 196
QY 207 ACGGTCTTTCATCAGCGGCACAGCCAGGGGGGAGAGAGATGCTGCTGCTCCTCAGA 266
DB 197 ACGGTCTTTCATCAGCGGCACAGCCAGGGGGGAGAGAGATGCTGCTGCTCCTCAGA 256
QY 267 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
DB 257 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
QY 327 CTACGCGCCGCTCGGCGCCACCGACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 386
DB 317 CTACGCGCCGCTCGGCGCCACCGACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 376
QY 387 CTTTCCACCGCTTCAGCGCCACCTATCGTACCTGACGACGAGATCGAAGTCCACCCAC 446
DB 377 CTTTCCACCGCTTCAGCGCCACCTATCGTACCTGACGACGAGATCGAAGTCCACCCAC 436
QY 447 CATCTGCTGCTCAGACGGGGAGAGGCCCCACCTTACAGGGGCCCCCTGACCCCTCAGCT 506
DB 437 CATCTGCTGCTCAGACGGGGAGAGGCCCCACCTTACAGGGGCCCCCTGACCCCTCAGCT 496

RESULT 13

US-10-872-972-44

; Sequence 44, Application US/10872972

; Publication No. US2004029277A1

; GENERAL INFORMATION:

; APPLICANT: Frantz, Gretchen

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Phillips, Heidi

; APPLICANT: Polakis, Paul

; APPLICANT: Spencer, Susan

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wu, Thomas

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF TUMOR

; FILE REFERENCE: P5010R1-US

; CURRENT APPLICATION NUMBER: US/10/872,972

; CURRENT FILING DATE: 2004-06-21

; PRIOR APPLICATION NUMBER: US/10/241,220

; PRIOR FILING DATE: 2002-09-11

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 44

; LENGTH: 1850

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-872-972-44

Query Match 87.6%; Score 754.2; DB 18; Length 1850;

Best Local Similarity 98.3%; Pred. No. 3.3e-191;

Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTGTGTTCCAGAGCATCGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTGTTGT 146
DB 77 TCTCCTCGGAACAGGCAATGGGAGCTGGAGTTGTTTCAGATCATCATCTGTTGT 136
QY 147 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 206
DB 137 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 196
QY 207 ACGGTCTTTCATCAGCGGCACAGCCAGGGGGGAGAGAGATGCTGCTGCTCCTCAGA 266
DB 197 ACGGTCTTTCATCAGCGGCACAGCCAGGGGGGAGAGAGATGCTGCTGCTCCTCAGA 256
QY 267 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
DB 257 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316

QY 327 CTACGCCCGCTCGGCCACCGACCGCTGGCGGTGGCGCCCTTCGCCACGCGGAGCG 386
Db 317 CTACGCCCGCTCGGCCACCGACCGCTGGCGGTGGCGCCCTTCGCCACGCGGAGCG 376
QY 387 CTTCCACCGCTTCAGCGCCACCTATCGTACTCTCAGCAGCAGATCGACCTGCCACCCAC 446
Db 377 CTTCCACCGCTTCAGCGCCACCTATCGTACTCTCAGCAGCAGATCGACCTGCCACCCAC 436
QY 447 CATCTCGCTGTCAGACGCGGAGGAGCCCAACCTTACGAGGCGCCCTGCACCCCTCCAGCT 506
Db 437 CATCTCGCTGTCAGACGCGGAGGAGCCCAACCTTACGAGGCGCCCTGCACCCCTCCAGCT 496
QY 507 TCGGAGCCCGCAGCAGCTGGAACCTGAACCCGAGTCTGGTGGCGCACCCCAACAG 566
Db 497 TCGGAGCCCGCAGCAGCTGGAACCTGAACCCGAGTCTGGTGGCGCACCCCAACAG 556
QY 567 AACCATCTTCAGACAGTCACTGATGATAGTGGAGGAGCCCGAGTGGCGGCCCTCCAGCT 626
Db 557 AACCATCTTCAGACAGTCACTGATGATAGTGGAGGAGCCCGAGTGGCGGCCCTCCAGCT 616
QY 627 CAGTAACTCGGGCATCAGCGCACCTGTACTAGCGCAGCGCGGCGCATGGAGGCGCGCC 686
Db 617 CAGTAACTCGGGCATCAGCGCACCTGTACTAGCGCAGCGCGGCGCATGGAGGCGCGCC 676
QY 687 GCCCACTACAGCAGCTCATCGGCCACTACTACCGGGGTCTCTTCAGCAGCAGCAGAG 746
Db 677 GCCCACTACAGCAGCTCATCGGCCACTACTACCGGGGTCTCTTCAGCAGCAGCAGAG 736
QY 747 CAGTGGCGCGCCCTCTTGTGGAGGAGCCCGGCTCCACACACACACACACACATCGGCCCT 806
Db 737 CAGTGGCGCGCCCTCTTGTGGAGGAGCCCGGCTCCACACACACACACACACATCGGCCCT 796
QY 807 AGAGAGCGAGCCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCCCTCTC 861
Db 797 AGAGAGCGAGCCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCCCTCTC 851

RESULT 14

US-10-872-991-44
; Sequence 44, Application US/10872991
; Publication No. US20040242860A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872,991
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-991-44

Query Match 87.6%; Score 754.2; DB 18; Length 1850;
Best Local Similarity 98.3%; Pred. No. 3.3e-191;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 87 TTTGTTCCAGAGCATCGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTGTGT 146
Db 77 TCTCTCGCAAAACAGGCAATCGGAGCTGGAGTTTGTTCAGATCATCATCTGTGT 136
QY 147 GGTGATGATGGTGTGATGATCAGTGGCGCTGAGCCACTACAGCTGTCTGC 206

Db 137 GGTGATGATGGTGTGATGATCAGTGGTGTGATCAGTGGCTGTGAGCACTACAAGCTGTCTGC 196
QY 207 ACAGTCTCTTCATCAGCCGCGCACAGCAGGCGGAGGAGAGAGATGCTCTGTCTCAGA 266
Db 197 ACAGTCTCTTCATCAGCCGCGCACAGCAGGCGGAGGAGAGAGATGCTCTGTCTCAGA 256
QY 267 AGGATGCTGTGGCCCTTCGAGAGAGCAGTGTTCAGCAACCGAATCCAGAGCGCAGGT 326
Db 257 AGGATGCTGTGGCCCTTCGAGAGAGCAGTGTTCAGCAACCGAATCCAGAGCGCAGGT 316
QY 327 CTACGCCCGCTTCGCCCGCACCGACCGCTGGCGGTGGCGCCCTTCGCCACGCGGAGCG 386
Db 317 CTACGCCCGCTTCGCCCGCACCGACCGCTGGCGGTGGCGCCCTTCGCCACGCGGAGCG 376
QY 387 CTTCCACCGCTTCAGCGCCACCTATCTCGTACTCTTCAGCAGCAGATCGACCTGCCACCCAC 446
Db 377 CTTCCACCGCTTCAGCGCCACCTATCTCGTACTCTTCAGCAGCAGATCGACCTGCCACCCAC 436
QY 447 CATCTCGCTGTCAGACGCGGAGGAGCCCGACCTTACAGGCGCCCTGCACCCCTCCAGCT 506
Db 437 CATCTCGCTGTCAGACGCGGAGGAGCCCGACCTTACAGGCGCCCTGCACCCCTCCAGCT 496
QY 507 TCGGAGCCCGCAGCAGCTGGAACCTGAACCGGAGTCTGGTGGCGCACCCCAACAG 566
Db 497 TCGGAGCCCGCAGCAGCTGGAACCTGAACCGGAGTCTGGTGGCGCACCCCAACAG 556
QY 567 AACCATCTTCAGACAGTCACTGATGATAGTGGAGGAGCCCGAGTGGCGGCCCTCCAGCT 626
Db 557 AACCATCTTCAGACAGTCACTGATGATAGTGGAGGAGCCCGAGTGGCGGCCCTCCAGCT 616
QY 627 CAGTAACTCGGGCATCAGCGCACCTGTACTAGCGCAGCGCGGCGCATGGAGGCGCGCC 686
Db 617 CAGTAACTCGGGCATCAGCGCACCTGTACTAGCGCAGCGCGGCGCATGGAGGCGCGCC 676
QY 687 GCCCACTACAGCAGCTCATCGGCCACTACTACCGGGGTCTCTTCAGCAGCAGCAGAG 746
Db 677 GCCCACTACAGCAGCTCATCGGCCACTACTACCGGGGTCTCTTCAGCAGCAGCAGAG 736
QY 747 CAGTGGCGCGCCCTCTTGTGGAGGAGCCCGGCTCCACACACACACACACATCGGCCCT 806
Db 737 CAGTGGCGCGCCCTCTTGTGGAGGAGCCCGGCTCCACACACACACACACATCGGCCCT 796
QY 807 AGAGAGCGAGCCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCCCTCTC 861
Db 797 AGAGAGCGAGCCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCCCTCTC 851

RESULT 15

US-09-821-812-2
; Sequence 2, Application US/09821812
; Publication No. US20030166520A1
; GENERAL INFORMATION:
; APPLICANT: Lin, BiaoYang
; TITLE OF INVENTION: Androgen Regulated Prostate Specific
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE: P-15 4373
; CURRENT APPLICATION NUMBER: US/09/821,812
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96) ... (851)
US-09-821-812-2

Query Match 87.6%; Score 754.2; DB 10; Length 4527;
Best Local Similarity 98.3%; Pred. No. 3.8e-191;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 10:31:50 ; Search time 2707.69 Seconds
(without alignments)
12103.794 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcacgcttgatgggggt.....aacagaaaggacacccctctc 861

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	811.8	94.3	1005	1	AL578575
c 2	807.6	93.8	1038	1	AL517150
c 3	743.6	86.4	967	5	BQ641849
c 4	700	81.3	1046	5	BM922276
c 5	693	80.5	901	3	CR612083
c 6	687.8	79.3	945	5	BUS39219
c 7	686.2	79.7	850	1	AL558881
c 8	667.4	77.5	916	5	BQ954555
c 9	667	77.5	867	5	BX362396
c 10	666.6	77.4	897	1	AL558882
c 11	662.8	77.0	850	5	BUE02918
c 12	648	75.3	780	9	AY419334
c 13	614.6	71.4	1079	3	BC023092
c 14	607.4	70.5	609	5	BQ636742
c 15	603.6	70.1	1207	3	AK008976
c 16	588.8	68.4	605	7	CV028567
c 17	578.4	67.2	890	5	BQ690750
c 18	570.4	66.2	973	5	BUI69156
c 19	568.8	66.1	572	5	BX641317
c 20	568.2	66.0	782	5	BQ015170
c 21	550	63.9	551	4	BM141979
c 22	529.8	61.5	894	4	BI851941
c 23	519.4	60.3	729	5	BQ575741
c 24	516.8	60.0	730	4	BM677602

c 25	515.2	59.8	728	5	BU683523
c 26	504	58.5	780	9	AY419335
c 27	501.6	58.3	588	4	BM483503
c 28	487.8	56.7	1059	1	AL543170
c 29	487.6	56.6	646	9	CG784226
c 30	475.2	55.2	624	9	AY419336
c 31	468	54.4	857	4	BG323347
c 32	465.8	54.1	744	5	BU414421
c 33	461	53.5	763	4	BI646175
c 34	445.6	51.8	693	1	AI761441
c 35	445.4	51.7	655	5	BQ691705
c 36	445.4	51.7	1280	5	BQ691500
c 37	443.6	51.5	651	6	CB554226
c 38	440	51.1	899	5	BUI69912
c 39	432.8	50.3	964	5	BUS59860
c 40	430	49.9	841	4	BI156703
c 41	429.6	49.9	646	5	BUS59841
c 42	428.8	49.8	974	2	BB624904
c 43	428.2	49.7	655	4	BI853324
c 44	416.2	48.3	587	4	BI083462
c 45	411.6	47.8	1127	5	BUI74654

ALIGNMENTS

RESULT 1
AL578575/c
LOCUS
DEFINITION
AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK001YC24 3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL578575 1005 bp mRNA linear EST 07-APR-2004
CDNA clone CS0DK001YC24 3-PRIME, mRNA sequence.
AL578575 GI:46257448
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31316780.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DK001B12NP1&c=9945.r.

FEATURES

source
1..1005
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK001YC24"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 94.3%; Score 811.8; DB 1; Length 1005;
Best Local Similarity 97.7%; Pred. No. 9.9e-170;
Matches 835; Conservative 8; Mismatches 10; Indels 2; Gaps 2;


```
QY 349 GACCGCTGCGCGCTGCGCGCTTGGCCCGCAGGGAGCGCTTCCACCGCTTCCAGCCACC 408
Db 181 GACCGCTGCGCGCTGCGCGCTTGGCCCGCAGGGAGCGCTTCCACCGCTTCCAGCCACC 240
QY 409 TATCCGTACCTGACGACGAGATGCGACCTCCACCCACCACTATCGCTGTCAGACGGGAG 468
Db 241 TATCCGTACCTGACGACGAGATGCGACCTCCACCCACCACTATCGCTGTCAGACGGGAG 300
QY 469 GAGCCCCACCTTACACAGGCGCCCTGACCGCTTCCAGCTTCGGGACCCCGAGCAGCAGTG 528
Db 301 GAGCCCCACCTTACACAGGCGCCCTGACCGCTTCCAGCTTCGGGACCCCGAGCAGCAGTG 360
QY 529 GAATGAAACCGGAGTCGCTGCGGCGACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 588
Db 361 GAATGAAACCGGAGTCGCTGCGGCGACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 589 ATGGATAGTCCAGGCTGCGGCGCCCTGCGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAG 648
Db 421 ATGGATAGTCCAGGCTGCGGCGCCCTGCGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 649 ACCTGCTACGCGAGCGCGCGCATGGAGGGCGCGCGCCCGGAGGAGGAGGAGGAGGAGGAG 708
Db 481 ACCTGCTACGCGAGCGCGCGCATGGAGGGCGCGCGCCCGGAGGAGGAGGAGGAGGAGGAG 540
QY 709 GGCACACTACCGGGGTCCTCTTCCAGCACCAGAGCAGTGGGCGCGCCCTCTCTTGGCTG 768
Db 541 GGCACACTACCGGGGTCCTCTTCCAGCACCAGAGCAGTGGGCGCGCCCTCTCTTGGCTG 600
QY 769 GAGGGGACCGGCTCCACACACACACATCGCGCCCTAGAGAGCGGAGGAGGAGGAGGAGGAG 828
Db 601 GAGGGGACCGGCTCCACACACACACATCGCGCCCTAGAGAGCGGAGGAGGAGGAGGAGGAG 660
QY 829 AAAGAGAGGATAAACAGAAAGGACACCCCTCTC 861
Db 661 AAAGAGAGGATAAACAGAAAGGACACCCCTCTC 693
```

RESULT 6

```
BU539219
LOCUS AGENCOURT_10215265 NIH_MGC_107 Homo sapiens cDNA clone
DEFINITION IMAGE:6569922 5', mRNA sequence.
```

```
ACCESSION BU539219
```

```
VERSION BU539219.1 GI:22849660
```

```
KEYWORDS EST.
```

```
SOURCE Homo sapiens (human)
```

```
ORGANISM Homo sapiens
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
```

```
TITLE NIH-MGC http://mgi.nci.nih.gov/
```

```
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
```

```
COMMENT Unpublished (1999)
```

```
CONTACT: Robert Strausberg, Ph.D.
```

```
EMAIL: cgapbs-remail.nih.gov
```

```
TISSUE Tissue Procurement: ATCC
```

```
CDNA cDNA Library Preparation: Rubin Laboratory
```

```
CDNA cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
CLONE Cloning by: Agencourt Bioscience Corporation
```

```
/clone lib="NIH_MGC_107"
```

```
/notes="Organ: breast; Vector: pOTB7; Site: 1: EcoRI;
```

```
Site 2: XhoI; cDNA made by oligo-dT priming.
```

```
Directionally cloned into EcoRI/XhoI sites using the
```

```
following 5' adaptor: GGACGAG(G). Library constructed by
```

```
Ling Hong in the laboratory of Gerald M. Rubin (University
```

```
of California, Berkeley) using ZAP-cDNA synthesis kit
```

```
(Stratagene) and Superscript II RT (Life Technologies).
```

```
Note: this is a NIH_MGC Library."
```

ORIGIN

```
Query Match 79.9%; Score 687.8; DB 5; Length 945;
Best Local Similarity 96.8%; Pred. No. 3.4e-142;
Matches 734; Conservative 0; Mismatches 23; Indels 3; Gaps 3;
QY 87 TTTTGTTCAGAGATCGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 146
Db 65 TCTCTCGGAAACACAGGCAATCGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 124
QY 147 GGTGATGATGTTGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 206
Db 125 GGTGATGATGTTGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 184
QY 207 ACGTCTCTTCATCAGCGCGCACAGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 266
Db 185 ACGTCTCTTCATCAGCGCGCACAGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 244
QY 267 AGGATGCTGTGTCGCTTCGGAGAGCAGTGTTCAGGCAACGGAATCCAGAGCGCAGGT 326
Db 245 AGGATGCTGTGTCGCTTCGGAGAGCAGTGTTCAGGCAACGGAATCCAGAGCGCAGGT 304
QY 327 CTACGCGCGCGCTTCGGCGCACACCGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 386
Db 305 CTACGCGCGCGCTTCGGCGCACACCGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 364
QY 387 CTTCACCGCTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446
Db 365 CTTCACCGCTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 424
QY 447 CATCTCGCTGTTCAGAGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 506
Db 425 CATCTCGCTGTTCAGAGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 484
QY 507 TCGGGAACCGCGAGCAGAGCTGGAACCTGAACCGGAGTGGTGGCGGCAACCCCAACAG 566
Db 485 TCGGGAACCGCGAGCAGAGCTGGAACCTGAACCGGAGTGGTGGCGGCAACCCCAACAG 544
QY 567 AACCATCTTCGACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 626
Db 545 AACCATCTTCGACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 604
QY 627 CAGTAACTCGGGCATCAGCGCCACGTCGTCAGCGGCGCGCGCGCGCGCGCGCGCGCG 686
Db 605 CAGTAACTCGGGCATCAGCGCCACGTCGTCAGCGGCGCGCGCGCGCGCGCGCGCGCG 664
QY 687 GCCCACTACAGAGAGTCAATCGGCGCACCTACCGCGGCTCTCTTCAGCAGCAGCAGAG 746
Db 665 GCCCACTACAGAGAGTCAATCGGCGCACCTACCGCGGCTCTCTTCAGCAGCAGCAGAG 724
QY 747 CAGTGGCGCGCGCT-CCTTGTCTGGAGGAGGAGCGGCTCCACACACACACATCGCG-CCC 804
Db 725 CAGTGGCGCGCGCT-CCTTGTCTGGAGGAGGAGCGGCTCCACACACACACATCGCG-CCC 784
QY 805 CTAGAGAGCGCAG-CCATCTCTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
Db 785 CTAGAGAGCGCAGCGCCATCTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 824
```

RESULT 7

```
AL558881/c
```

```
LOCUS
```

```
DEFINITION
```

```
AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
```

```
850 bp mRNA linear EST 02-APR-2004
```

```
Homo sapiens cDNA clone CS0J015YF12 3-PRIME, mRNA sequence.
```

FEATURES

```
source
```

```
1. .945
```

```
/organism="Homo sapiens"
```

```
/mol_type="mRNA"
```

```
/db_xref="taxon:9606"
```

```
/clone="IMAGE:6569922"
```

```
/tissue_type="adenocarcinoma, cell line"
```

```
/lab_host="DH10B (phage-resistant)"
```


QY 810 GAGCGACCCATCTGGAGCAAGAGAGATATAACAGAAAGGACACCCCTCTC 861
 |||||
 Db 208 GAGCGACCCATCTGGAGCAAGAGAGATATAACAGAAAGGACACCCCTCTC 157
 |||||

RESULT 10
 AL558882
 LOCUS
 DEFINITION 897 bp mRNA linear EST 02-APR-2004
 AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 Homo sapiens cDNA clone CS0DJ015VF12 5-PRIME, mRNA sequence.
 AL558882
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

On Feb 15, 2001 this sequence version replaced gi:31283015.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0DJ015DC06QP1&c=9945.r.

FEATURES
 source
 Location/Qualifiers
 1..897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ015VF12"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /call_line="JURKAT"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 77.4%; Score 666.6; DB 1; Length 897;
 Best Local Similarity 99.3%; Pred. No. 1.7e-137;
 Matches 688; Conservative 2; Mismatches 1; Indels 2; Gaps 2;
 169 GTGATCAGCGTCTGTGACGCACTACAGCTGTGCGCGTCTTATCAGCGGCAC 228
 1 GTGATCAGCGTCTGTGACGCACTACAGCTGTGCGCGTCTTATCAGCGGCAC 60
 229 AGCCAGGGCGGAGGAGAGATGCTCTCTCTCAGAGAGATGCTGTGGCCCTCGGAG 288
 61 AGCCAGGGCGGAGGAGAGATGCTCTCTCTCAGAGAGATGCTGTGGCCCTCGGAG 120
 289 AGCACAGTGTACGCAACGAATCCAGAGCGCGAGTCTAGCGCCGCTCGGCCACC 348
 121 AGCACAGTGTACGCAACGAATCCAGAGCGCA-GTCTAGCGCCGCTCGGCCACC 179
 349 GACCGCTGCGGTGCGGCGCTTCGCCAGCGGAGCGCTTCAACGCTTCAGGCCACC 408
 180 GACCGCTGCGGTGCGGCGCTTCGCCAGCGGAGCGCTTCAACGCTTCAGGCCACC 239
 409 TATCCGTACTGTGACGACGAGATGCACTGCGACCCACCACCATCTCGCTGTGACGGGAG 468
 |||||

Db 240 TATCCGTACTGTGACGACGAGATCGACCTCGGCCACCATCTCGCTGTGACGGGGAG 299
 QY 469 GAGCCCCCACCCTACACAGGGCCCTTGACCCCTCGAGTTCCGGGACCCCGAGCGAGCTG 528
 Db 300 GAGCCCCCACCCTACACAGGGCCCTTGACCCCTCGAGTTCCGGGACCCCGAGCGAGCTG 359
 QY 529 GAACTGAACCGGAGTGGTGGCGCACCCCAAGAACCAACCATCTTCGACAGTGACCTG 588
 Db 360 GAACTGAACCGGAGTGGTGGCGCACCCCAAGAACCAACCATCTTCGACAGTGACCTG 419
 QY 589 ATGATAGTATCCAGGCTGGCGGCCCTTGCCTCCAGCAGTAACTCGGGCCTACAGCGCC 648
 Db 420 ATGATAGTATCCAGGCTGGCGGCCCTTGCCTCCAGCAGTAACTCGGGCCTACAGCGCC 479
 QY 649 ACCTGTGTACGGCAGCGCGGCATGAGAGGGCGCCGCCACCTACAGCGAGTGCATC 708
 Db 480 ACCTGTGTACGGCAGCGCGGCATGAGAGGGCGCCGCCACCTACAGCGAGTGCATC 539
 QY 709 GGCACCTACCCCGGGTCTCTCTCCAGCAGCAGCAGCAGTGGCGCCCTCTTGTGCTG 768
 Db 540 GGCACCTACCCCGGGTCTCTCTCCAGCAGCAGCAGCAGTGGCGCCCTCTTGTGCTG 599
 QY 769 GAGGGACCCCGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGC 828
 Db 600 GAGGGACCCCGCTCCACACACATCGCGCCCTTAGAGAGCGCA-SCATCTGGAGC 658
 QY 829 AAAGAGAAGGATAAACAAGAGACACCCCTCTC 861
 Db 659 AAAGAGAAGGATAAACAAGAGACACCCCTCTC 691

RESULT 11
 BU602918
 LOCUS
 DEFINITION 850 bp mRNA linear EST 20-SEP-2002
 AGENCOURT_10016502 NIH_MGC_142 Homo sapiens cDNA clone
 IMAGE:6497853 5', mRNA sequence.
 BU602918
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1 (bases 1 to 850)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-romail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2679 row: 1 column: 22
 High quality sequence stop: 499.
 Location/Qualifiers
 1..850
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6497853"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (Tl-phage-resistant)"
 /clone_lib="NIH_MGC_142"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2% blood - 33.4% brain - 5.6% breast - 12.5% colon -
 4% connective tissue - 1.4% eye - 1% intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,

ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:

5'-AAGCAGTGGTATCAAGCAGCAGTGGCCATACGCGCGG-3' and 5'-ATTCTAGAGCGCGCGCGACATG-dt(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH_MGC_141). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 77.0%; Score 662.8; DB 5; Length 850;
Best Local Similarity 97.9%; Pred. No. 1.2e-136;
Matches 703; Conservative 0; Mismatches 12; Indels 3; Gaps 3;
QY 147 GGTGATGATGGTGTGGTGTGATCAGTGTGCTGAGCCACTACAAAGTGTCTGC 206
Db 1 GGTGATGATGGTGTGGTGTGATCAGTGTGCTGAGCCACTACAAAGTGTCTGC 60
QY 207 ACGGTCTTTCATCAGCGCGCACAGCGCGGCGGAGAGAGATGCTGTCTTCAGA 266
Db 61 ACGGTCTTTCATCAGCGCGCACAGCGCGGCGGAGAGAGATGCTGTCTTCAGA 120
QY 267 AGGATGCTGTGCGCTCGGAGGACACAGTGTGAGCAACGGAATCCAGAGCGGAGT 326
Db 121 AGGATGCTGTGCGCTCGGAGGACACAGTGTGAGCAACGGAATCCAGAGCGGAGT 180
QY 327 CTACGCGCGCGCTCGCGCCACCGCTGCGCGCTGCGCGCTGCGCGCGGAGCG 386
Db 181 CTACGCGCGCGCTCGCGCCACCGCTGCGCGCTGCGCGCTGCGCGCGGAGCG 240
QY 387 CTTTCCACCGCTTCCAGCGCACCTTATCGTACCTGCGACGACGAGATCGACCTGCCAC 446
Db 241 CTTTCCACCGCTTCCAGCGCACCTTATCGTACCTGCGACGACGAGATCGACCTGCCAC 300
QY 447 CATCTCGTGTACAGCGGAGAGAGCGCCACCTTACCGGCGCGCTGCAACCTTCAGT 506
Db 301 CATCTCGTGTACAGCGGAGAGAGCGCCACCTTACCGGCGCGCTGCAACCTTCAGT 360
QY 507 TCGGGACCGCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGCGACCCCAACAG 566
Db 361 TCGGGACCGCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGCGACCCCAACAG 420
QY 567 AACCATCTTCGACAGTGAACCTGATAGTGCAGCTGGCGCGCGCTGCCCGCCAG 626
Db 421 AACCATCTTCGACAGTGAACCTGATAGTGCAGCTGGCGCGCGCTGCCCGCCAG 480
QY 627 CAGTAACTCGGGATCAGCGCCACGTCGTACCGGAGCGCGCGCGATGAGGGCGCGC 686
Db 481 CAGTAACTCGGGATCAGCGCCACGTCGTACCGGAGCGCGCGCGATGAGGGCGCGC 540
QY 687 GCCCACTACAGGAGTATCGGCGACCTACCGGGGTCTCTCCAGCAGCAGAG 746
Db 541 GCCCACTACAGGAGTATCGGCGACCTACCGGGGTCTCTCTCCAGCAGCAGAG 600
QY 747 CAGTGGCGCG-CCCTCTTCTCTG-AGGGGACCGCGCTCCACACACACATCGCGCCC 804
Db 601 CAGTGGCGCGCCCTCTTCTCTGAGGGGACCGGTTCCACACACACATCGCGCCC 660
QY 805 CTAGAGAGCGCAGCCA-TCCTGGAGCAAGAGAGGATAAACAGAGGACCTCTC 861
Db 661 CTAAGAGCGCAGCCATTCTGGAGCAAGCAGATGATTAACCGAAGGACCCCTCTC 718

RESULT 12

AY419334
LOCUS
DEFINITION Homo sapiens TMEPAI gene, 780 bp DNA linear GSS 17-DEC-2003
genomic survey sequence.
ACCESSION AY419334
VERSION AY419334.1 GI:39775291
KEYWORDS GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 780)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 780)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source 1..780
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1..>780
/gene="TMEPAI"
/locus_tag="HCM6856"
ORIGIN
Query Match 75.3%; Score 648; DB 9; Length 780;
Best Local Similarity 86.2%; Pred. No. 2.3e-133;
Matches 648; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 110 CGAGTGTGAGTTTGTTCAGATCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTG 169
Db 26 CGAGTGTGAGTTTGTTCAGATCATCATCTGTGTGTGTGTGTGTGTGTGTGTGTG 85
QY 170 TGATCAGTGTCTGT 229
Db 86 TGATCAGTGTCTGT 145
QY 230 GCCAGGGCGGAGAGAGAGATGCGCTGTCTCAGAGGATGCTGTGTGTGTGTGTGTGT 289
Db 146 GCCAGGGCGGAGAGAGAGATGCGCTGTCTCAGAGGATGCTGTGTGTGTGTGTGTGT 205
QY 290 GCACAGTGTGAGCAACGGAATCCAGAGCGCGAGTCTACGCCCGCTTCGGCCCAACCG 349
Db 206 GCACAGTGTGAGCAACGGAATCCAGAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNN 265
QY 350 ACGGCTGTGCGGTGCGCGCTTCGCCCGAGGAGCGCTTCACCGCTTCACGCCACCT 409
Db 266 NNN 325
QY 410 ATCCGTACCTGCAGCAGCAGATCGACCTGCACCCACCATCTCGTGTGTGTGTGTGTGT 469
Db 326 NNN 385
QY 470 AGCCCCCACCCTACCAAGGGCCCCGTGCACCTTCAGCTTCGGGACCCCGAGCAGCAGTGG 529
Db 386 AGCCCCCACCCTACCAAGGGCCCCGTGCACCTTCAGCTTCGGGACCCCGAGCAGCAGTGG 445
QY 530 AACTGAACCGGAGTGTGCGGCGACCCCGCAACCAAGACCATCTTCGACAGTGA 589
Db 446 AACTGAACCGGAGTGTGCGGCGACCCCGCAACCAAGACCATCTTCGACAGTGA 505
QY 590 TGGATAGTCCAGGCTGGGCGGCGCCCTGCCCGCCAGCAGTAACTCGGGCATCAGGCCCA 649
Db 506 TGGATAGTCCAGGCTGGGCGGCGCCCTGCCCGCCAGCAGTAACTCGGGCATCAGGCCCA 565

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL REFERENCE
 Nature 420, 563-573 (2002)

AUTHORS
 6 (bases 1 to 1207)
 Adech, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE
 Direct Submission

JOURNAL
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT
 Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGACTCTTTTCTTTTCTTTTWN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGAGTATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
 Host: SOLR.

FEATURES
 Location/Qualifiers
 1..1207
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:2210418102"
 /db_xref="taxon:10090"
 /clone="2210418102"
 /sex="male"
 /tissue_type="stomach"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="adult"
 391..1173
 /notes="unnamed protein product; Nedda WW binding protein 4 (MCD|WGI:1923600)
 putative"
 /codon_start=1
 /protein_id="BAB26001.1"
 /db_xref="GI:12843489"
 /tranlations="MSPARATQSLRFPSPMEITELFQVIVIVVWVWVMTCLLAV SHYKLSARFPISRHQARRDDGSEGCCLWPSESTVSGMPPEQVATPPRPDRLIAV PPIQRNRQPTPYLOHETALPTTSLSDGEEPPPYQGGCTQLQDLPEQQLRINRS VAPPNRTTFLDSLIDTWMLGSGPPFSNSGIGSTVSGGRMEGPPPTYSRVIGHYP GSSFRQOQSGNPSSLLEGTRLHHSHTAPLENKEKEKQKGPL"

CDS
 Query Match
 Best Local Similarity 70.1%; Score 603.6; DB 3; Length 1207;
 Matches 731; Conservative 0; Mismatches 99; Indels 28; Gaps 4;

ORIGIN
 5 ACCGCTTGATGGGGGTCAACAGCACCGCCGCCGCCGCCGGGCGAGCCCAATGCTCTCCT 64
 340 ACCGCTTGATGGGGGTCAACGGCACCGCCGCCGCCGCCGGGCGAGCCCAATGCTCTCCT 399
 65 GCACGTGCAACTG-CAAAAGCTCTTTTGTTCAGAGCATGGAGATCATGGAGCTGGAGTTT 123

Result No.	Score	Query		Length	DB	ID	Description
		Match	Time				
1	861	100.0	861	6	AX392419	Sequence	
2	861	100.0	1321	6	AX392417	Sequence	
3	861	100.0	4839	6	Q0812357	Sequence	
4	861	100.0	4839	9	AF305616	Homo sapi	
5	861	94.1	1383	6	AX775889	Sequence	
6	790	91.8	1061	9	BC015918	Homo sapi	
7	752	87.3	759	6	AR336831	Sequence	
8	752	87.3	1140	6	AR336830	Sequence	
9	752	87.3	1141	9	AF224218	Homo sapi	
10	752	87.3	1818	9	AY128643	Homo sapi	
11	701	81.4	753	6	BD272534	Secreted	
12	701	81.4	756	6	BD272495	Secreted	
13	701	81.4	759	6	BD272545	Secreted	
14	701	81.4	969	6	BD272494	Secreted	
15	701	81.4	1085	6	AX775887	Sequence	
16	701	81.4	1913	6	BD272544	Secreted	
17	696	80.8	969	6	BD272514	Secreted	
18	650	75.5	969	6	BD272515	Secreted	
19	650	75.5	969	6	BD272516	Secreted	

Qy	481	TACAGGGCCCTGCACCCTTCAGCTTTCGGGACCCCAGCAGCAGCTGGAACTGAACCGG	540
Dd	801	TACAGGGCCCTTCGCAACCTTCAGCTTTCGGGACCCCAGCAGCAGCTGGAACTGAACCGG	860
Qy	541	GAGTCGGTGCGCGCACCCCCAACAAGAACCATCTTCGACAGTAGCCTGTATGGATAGTGCC	600
Dd	861	GAGTCGGTGCGCGCACCCCCAACAAGAACCATCTTCGACAGTAGCCTGTATGGATAGTGCC	920
Qy	601	AGGTCGGGCGGCCCTTCGCCGCCCCAGCAGTAACCTCGGGCATCAGCGCCACTGCTACGGC	660
Dd	921	AGGTCGGGCGGCCCTTCGCCGCCCCAGCAGTAACCTCGGGCATCAGCGCCACTGCTACGGC	980
Qy	661	AGCGGGGCGCGCATGAGAGGGGCGCGCCGCCACTTACAGCGAGTCACTCGGCCACTACCGG	720
Dd	981	AGCGGGGCGCGCATGAGAGGGGCGCGCCGCCACTTACAGCGAGTCACTCGGCCACTACCGG	1040
Qy	721	GGTCTCTCTTCAGCAGCAGCAGCAGTAGGGGCGCGCCCTCTCTCTCTGGAGGGGACCGCG	780
Dd	1041	GGTCTCTCTTCAGCAGCAGCAGCAGTAGGGGCGCGCCCTCTCTCTCTGGAGGGGACCGCG	1100
Qy	781	CTCCACCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAAGAAGAGAT	840
Dd	1101	CTCCACCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAAGAAGAGAT	1160
Qy	841	AAACAGAAAGGACACCTCTCTC	861
Dd	1161	AAACAGAAAGGACACCTCTCTC	1181
RESULT 4			
AF305616			
LOCUS	AF305616	Homo sapiens STAG1/PMEPAl mRNA, complete cds.	PRI 21-OCT-2001
DEFINITION	AF305616		
ACCESSION	AF305616		
VERSION	AF305616.1	GI:16303741	
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 4839)	
JOURNAL		Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.	
MEDLINE		Characterization of a novel gene, STAG1/PMEPAl, upregulated in	
FURNED		renal cell carcinoma and other solid tumors	
AUTHORS		Mol. Cell Carcinog. 32 (1), 44-53 (2001)	
TITLE		Submitted (14-SEP-2000) Centre for Molecular Biotechnology,	
JOURNAL		Queensland University of Technology, 2 George St, Brisbane, QLD	
FEATURES		4001, Australia	
source		Location/Qualifiers	
CDS		1..4839	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/chromosome="20"	
		/map="20q13.2-q13.33"	
		321..1184	
		/notes="unknown function"	
		/codon_start=1	
		/product="STAG1/PMEPAl"	
		/protein_id="AAU16781.1"	
		/db_xref="GI:16303742"	
		/translation="MRLMGVNSTAAAAAQPNVSCNCKRSLFOSMBITTELEFVQI IIIVVMVVVITCLLGHYKLSARSPFSRSQGRREDALSEGLWPSESVTSVGNI GIPEQVAPPRDLPBPQAERHFPOPTYLOHEIDLPTISLDGEERP YQPCFLQRDPQELNRESVRAPPNTIFSDMLMSRLGCPGPSNSGISATC YSGSGRMGPPIYSYVIHYPGSSFPQQSSGPPSLLETTRLIHTIAPLBSAAIWS KEKDQKGHP"	

Db	861	GAGTCGGTCGGCGCACCCCAACAGAACCAATCTTTCAGACAGTACCTGTGATGAGATAGTGGCC	920
Qy	601	AGGCTGGCGCGCGCCCTGCTCCCGCCCGCAGCAGTAACCTCGGCGCATCAAGCGCCACGTCGTACGGC	660
Db	921	AGGCTGGCGCGCGCCCTGCTCCCGCCCGCAGCAGTAACCTCGGCGCATCAAGCGCCACGTCGTACGGC	980
Qy	661	AGCGCGCGGCGCATGAGAGGGCGCGCCGCCCACTTACAGCAGAGTCAATCGGCGCATACCCG	720
Db	981	AGCGCGCGGCGCATGAGAGGGCGCGCCGCCCACTTACAGCAGAGTCAATCGGCGCATACCCG	1040
Qy	721	GGGTCTCTTTCAGACACCAAGCAGAGTGGGCGCGCCCTCTTCTGCTGGAGGGAGCCCGG	780
Db	1041	GGGTCTCTTTCAGACACCAAGCAGAGTGGGCGCGCCCTCTTCTGCTGGAGGGAGCCCGG	1100
Qy	781	CTCCACCAACACACATCTCGGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGAGAT	840
Db	1101	CTCCACCAACACACATCTCGGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGAGAT	1160
Qy	841	AAACAGAAAGGACACCTCTC	861
Db	1161	AAACAGAAAGGACACCTCTC	1181
RESULT 6			
LOCUS	BC015918	1061 bp	linear
DEFINITION	Homo sapiens transmembrane, prostate androgen induced RNA, mRNA		
	(CDNA clone IMAGE:4559576), partial cds.		
ACCESSION	BC015918		
VERSION	BC015918.1	GI:16198474	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1061)		
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Viala, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBLISHED	12477932		
REFERENCE	2 (bases 1 to 1061)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgaps-x@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ruben Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequencing Centre, BC Cancer Agency, Vancouver, BC, Canada		


```

Db      181 GTCTGACGCTCTTTCATCAGCCGCGCAGCCAGGCGCGAGGAGAGATGCCCTCTC 240
Qy      261 CTCAGAGGATGCTCTGTCGCTCTCGGAGAGACAGTGTTCAGGCAACGAATCCAGAGCC 320
Db      241 CTCAGAGGATGCTCTGTCGCTCTCGGAGAGACAGTGTTCAGGCAACGAATCCAGAGCC 300
Qy      321 CGAGGTCTACGCGCGCTCTCGGCGCCACGACCGCTGCGCGCTGCGCGCTTTCGCGCAGCG 380
Db      301 GCAGGTCTACGCGCGCTCTCGGCGCCACGACCGCTGCGCGCTTTCGCGCAGCG 360
Qy      381 GGAGCGCTTTCACCGCTTTCAGCGCCACCTATCTCGTACCTGTCAGCAGAGATCGACCTGCC 440
Db      361 GGAGCGCTTTCACCGCTTTCAGCGCCACCTATCTCGTACCTGTCAGCAGAGATCGACCTGCC 420
Qy      441 ACCACCATCTCGCTGTTCAGACGGGAGGAGCGCCACCTACCGGCGCGCTTTCGACGCT 500
Db      421 GCCACCATCTCGCTGTTCAGACGGGAGGAGCGCCACCTACCGGCGCGCTTTCGACGCT 480
Qy      501 CCAGCTTCGGGACCCCGAGCAGCTGGAACCTGAACCGGAGTCTGCTGCGCGCACCCCC 560
Db      481 CCAGCTTCGGGACCCCGAGCAGCTGGAACCTGAACCGGAGTCTGCTGCGCGCACCCCC 540
Qy      561 AAACAGAACCATCTTCGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATG 620
Db      541 AAACAGAACCATCTTCGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATG 600
Qy      621 CCCAGCAGTAACTCGGGCATCAGCGCCACCTGCTACGCGAGTCTGCTGCGCGCACCCCC 680
Db      601 CCCAGCAGTAACTCGGGCATCAGCGCCACCTGCTACGCGAGTCTGCTGCGCGCACCCCC 660
Qy      681 CGCGCGCGCCACCTACAGCAGGAGTCTGCGCACTACCCGGGCTCTCTTTCAGCACCA 740
Db      661 CGCGCGCGCCACCTACAGCAGGAGTCTGCGCACTACCCGGGCTCTCTTTCAGCACCA 720
Qy      741 GCAGAGCAGTGGCGCGCTCTGCTGAGGAGACCGGCTTCCACACACACATCGC 800
Db      721 GCAGAGCAGTGGCGCGCTCTGCTGAGGAGACCGGCTTCCACACACACATCGC 780
Qy      801 GCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGAGATTAACAGAAAGGACACCTCT 860
Db      781 GCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGAGATTAACAGAAAGGACACCTCT 840
Qy      861 C 861
Db      841 C 841

```

```

RESULT 7
AR336831
LOCUS      AR336831      759 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6566130.
ACCESSION  AR336831
VERSION    AR336831.1  GI:33722681
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 759)
AUTHORS   Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE     Androgen-regulated gene expressed in prostate tissue
JOURNAL   Patent: US 6566130-A 2 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1. .759
               /organism="unknown"
               /mol_type="genomic DNA"
ORIGIN
Query Match      87.3%; Score 752; DB 6; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      110 CGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGCTGATGATGATGATGATGATGATG 169

```

```

Db      5   CGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGCTGATGATGATGATGATGATGATG 64
Qy      170 TGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 229
Db      65   TGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124
Qy      230 GCCAGGGGCGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 289
Db      125 GCCAGGGGCGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
Qy      290 GCACAGTGTTCAGCAACCGAATCCAGAGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
Db      185 GCACAGTGTTCAGCAACCGAATCCAGAGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
Qy      350 ACCGCTTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 409
Db      245 ACCGCTTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
Qy      410 ATCCGTACCTGCGACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469
Db      305 ATCCGTACCTGCGACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
Qy      470 AGCCCCACCTTACAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
Db      365 AGCCCCACCTTACAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
Qy      530 AACTGAACCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
Db      425 AACTGAACCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 484
Qy      590 TGGATAGTCCAGGCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
Db      485 TGGATAGTCCAGGCTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
Qy      650 CTGTGTACGCGAGCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
Db      545 CTGTGTACGCGAGCGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 604
Qy      710 GCCACTTACCGGGTCTCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 769
Db      605 GCCACTTACCGGGTCTCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 664
Qy      770 AGGGGACCGGCTCCACACACACACATCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
Db      665 AGGGGACCGGCTCCACACACACACATCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
Qy      830 AAGAGAGGATTAACAGAAAGGACACCTCTCTC 861
Db      725 AAGAGAGGATTAACAGAAAGGACACCTCTCTC 756

```

```

RESULT 8
AR336830
LOCUS      AR336830      1140 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6566130.
ACCESSION  AR336830
VERSION    AR336830.1  GI:33722680
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1140)
AUTHORS   Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE     Androgen-regulated gene expressed in prostate tissue
JOURNAL   Patent: US 6566130-A 1 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1. .1140
               /organism="unknown"
               /mol_type="genomic DNA"
ORIGIN
Query Match      87.3%; Score 752; DB 6; Length 1140;

```


QY 590 TGGATAGTCCAGGCTGGCGCCCTGCTGCCCCCAGCAGTAACATCGGGCATCAGCGCA 649
 |||||
 Db 580 TGGATAGTCCAGGCTGGCGCCCTGCTGCCCCCAGCAGTAACATCGGGCATCAGCGCA 639
 |||||
 QY 650 CQTGCTACGGCAGCGCGGCATGAGGGCCCGCCGCCACCTACAGCAGGTCATCG 709
 |||||
 Db 640 CQTGCTACGGCAGCGCGGCATGAGGGCCCGCCGCCACCTACAGCAGGTCATCG 699
 |||||
 QY 710 GCCACTACCCGGGTCCTCTTCCAGCACCAGCAGCAGTGGCGCCCTCTTGTGG 769
 |||||
 Db 700 GCCACTACCCGGGTCCTCTTCCAGCACCAGCAGCAGTGGCGCCCTCTTGTGG 759
 |||||
 QY 770 AGGGAGCCCGGCTCCACACACACATCGCGCCCTAGAGAGCGCACCATCTGGAGCA 829
 |||||
 Db 760 AGGGAGCCCGGCTCCACACACACATCGCGCCCTAGAGAGCGCACCATCTGGAGCA 819
 |||||
 QY 830 AAGAGAAGGATAAAGAGAGGACCCCTCTC 861
 |||||
 Db 820 AAGAGAAGGATAAAGAGAGGACCCCTCTC 851
 |||||

RESULT 10
 LOCUS AY128643 1818 bp mRNA linear PRI 10-APR-2003
 DEFINITION Homo sapiens PMEPAL variant A protein mRNA, complete cds.
 ACCESSION AY128643
 VERSION AY128643.1 GI:22121998
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1818)
 Bruntschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E.,
 Willson, J.K.V., Lu, S., Nosrati, A., Reko, R.M., Swinler, S., Beard, L.,
 Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S.
 PMEPAL, a transforming growth factor-beta-induced marker of
 terminal colonocyte differentiation whose expression is maintained
 in primary and metastatic colon cancer
 Cancer Res. 63 (7), 1568-1575 (2003)
 2257253
 12670906
 2 (bases 1 to 1818)
 Bruntschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E.,
 Willson, J.K.V., Lu, S., Nosrati, A., Swinler, S., Beard, L.,
 Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S.
 Direct Submission
 Submitted (03-JUL-2002) Department of Medicine, Case Western
 Reserve University/Howard Hughes Medical Institute, 11001 Cedar
 Ave., Cleveland, OH 44106, USA
 Location/Qualifiers
 1. 1818
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="20"
 /map="20q13.31-13.33"
 145..858
 /codon_start=1
 /product="PMEPAL variant A protein"
 /protein_id="AA089277.1"
 /db_xref="GI:22121998"
 /translations="MMWVVVITCLSHYKLSARSPISRHSGRRRDLSSGCLMP
 SEVTSNGNIPQVYAPRPRDRLAVPFAQRFRFPQPTLYLQHEIDLPPTISL
 SDGEPPFYQGLQRLRDEQOELNRESVRPNRTIFDSDLMDLARLGGPCPPSS
 NSGISATCYSGSGMEGPPPTYSVIGHYPGSGFQHQSSGPPSLLEGTRLHHTHIAP
 LESAALWSKDKQKGHPL"

FEATURES
 source

CDS

BD272534 753 bp DNA linear PAT 17-JUL-2003
 Secreted proteins and nucleic acids encoding them.
 BD272534
 BD272534.1 GI:33082302
 JP 2002539773-A/43.
 Homo sapiens (human)
 Homo sapiens
 ORGANISM

REFERENCE
 1 (bases 1 to 753)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 753)
 Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
 Secreted proteins and nucleic acids encoding them
 Patent: JP 2002539773-A 43 26-NOV-2002;
 MILLENNIUM PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002539773-A/43
 PD 26-NOV-2002
 PF 01-MAR-2000 JP 2000602247

ORIGIN

Query Match 87.3%; Score 752; DB 9; Length 1818;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR	01-MAR-1999 US	60/122458
PI	THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER	
PC	C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15,	
PC	G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC Secreted proteins and nucleic acids encoding them FH Key	
	Location/Qualifiers	
FT	source	1..753
FT	source	/organism='Homo sapiens (human)'. Location/Qualifiers 1..753 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
FEATURES	source	
ORIGIN		
	Query Match	81.4%; Score 701; DB 6; Length 753;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 75;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	110 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGCTGCTCAGAAGGATGCCTGTGGCCCTCGGAGA	169
Db	2 CGGAGCTGGAGTTTGTTCAGATCATCATCGTGCTGCTCAGAAGGATGCCTGTGGCCCTCGGAGA	61
Qy	170 TGATCAGTGCCTGCTGAGCACCTACAACTGTCTGCAAGTGTCTGCAAGTCTTTCATCAGCCGGCACA	229
Db	62 TGATCAGTGCCTGCTGAGCACCTACAAAGTGTCTGCAAGTGTCTGCAAGTCTTTCATCAGCCGGCACA	121
Qy	230 GCCAGGGCGGAGGAGAGAGATGCCCTGTCTCAGAAGGATGCCTGTGGCCCTCGGAGA	289
Db	122 GCCAGGGCGGAGGAGAGATGCCCTGTCTCAGAAGGATGCCTGTGGCCCTCGGAGA	181
Qy	290 GCACAGTGTCAAGCAACGGGAATCCAGAGCGCAGAGTCTACGCCCCGCCCTGGCCCCACCG	349
Db	182 GCACAGTGTCAAGCAACGGGAATCCAGAGCGCAGAGTCTACGCCCCGCCCTGGCCCCACCG	241
Qy	350 ACCGCTTGGCGTGCCTTTCGCCCGAGCGGGAGCGCTTCCACCGCTTCCAGCCGACCT	409
Db	242 ACCGCTTGGCGTGCCTTTCGCCCGAGCGGGAGCGCTTCCACCGCTTCCAGCCGACCT	301
Qy	410 ATCCGTACTTGCAGCAGAGATGCACCTGCCACCACCATCTCGCTCTGCAGACGGGAGG	469
Db	302 ATCCGTACTTGCAGCAGAGATGCACCTGCCACCACCATCTCGCTCTGCAGACGGGAGG	361
Qy	470 AGCCCCAACCTTACAGGGCCCCCTGCACCTTCAGTCTCGGAGACCCCGAGCAGCAGTGG	529
Db	362 AGCCCCAACCTTACAGGGCCCCCTGCACCTTCCAGCTTCGGGAGCCCGAGCAGCAGTGG	421
Qy	530 AACGTAAACCGGAGTTCGGTGGCGGCACCCCAAACAGAACCATCTTTCGACAGTAGACCTGA	589
Db	422 AACGTAAACCGGAGTTCGGTGGCGGCACCCCAAACAGAACCATCTTTCGACAGTAGACCTGA	481
Qy	590 TGGATAGTGCAGAGCTGGGGCGGCCCTTGCCCCCCCAGCAGTAACCTCGGGGATCAGCGCCA	649
Db	482 TGGATAGTGCAGAGCTGGGGCGGCCCTTGCCCCCCCAGCAGTAACCTCGGGGATCAGCGCCA	541
Qy	650 CGTGCTACGGCAGCGGGCGGCATAGAGGGGGCGCGCCGCCCACTTACAGCGAGGTATCG	709
Db	542 CGTGCTACGGCAGCGGGCGGCATAGAGGGGGCGCGCCGCCCACTTACAGCGAGGTATCG	601
Qy	710 GCCTACTCCGGGGTCTCTTTCAGACACAGCAGCAGCAGTGGGGCGCCCTCTTGTCTGG	769
Db	602 GCCTACTCCGGGGTCTCTTTCAGACACAGCAGCAGCAGTGGGGCGCCCTCTTGTCTGG	661
Qy	770 AGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGGAGCA	829
Db	662 AGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGGAGCA	721
Qy	830 AAGAGAGGGATAAACAGAAAGGACACCCCTCTC	861
Db	722 AAGAGAGGGATAAACAGAAAGGACACCCCTCTC	753

RESULT 15	AX775887	LOCUS	AX775887	Sequence 157 from Patent WO03048202.	1085 bp mRNA	linear	PAT 14-JUL-2003		
DEFINITION	AX775887	ACCESSION	AX775887						
VERSION	AX775887.1	GI:32693605							
KEYWORDS									
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
650	CCTGCTACGGCAGCGCGCGGCATGAGAGGGGCGCCGCCACCTACAGCGAGGTCAATCG	Qy							709
672	CCTGCTACGGCAGCGCGCGGCATGAGAGGGGCGCCGCCACCTACAGCGAGGTCAATCG	Db							731
710	GCCACTACCCGGGGTCCTCTTCCAGCACACGAGAGAGCAGTGGGCGCCCTCTTGTGTGG	Qy							769
732	GCACTACCCGGGGTCCTCTTCCAGCACACGAGAGAGCAGTGGGCGCCCTCTTGTGTGG	Db							791
770	AGGGGACCCGGGTCACACACACATCGCGCCCTTAGAGAGCGCAGCCCATCTGGAGCA	Qy							829

Db 792 AGGGGACCCGGCTCCACCCACACACATGCGGCCCTAGAGAGCGCAGCCATCTGGAGCA 851
Qy 830 AAGAGAAGGATTAACAGAAAGGACACCCCTCTC 861
Db 852 AAGAGAAGGATTAACAGAAAGGACACCCCTCTC 883

Search completed: February 19, 2005, 22:03:58
Job time : 3716.3 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	861	100.0	864	11	ADN38809	Cancer/an
2	861	100.0	1321	6	AEK12137	Human CDN
3	861	100.0	4839	8	ACC49552	Tumour-as
4	861	100.0	4839	11	ADP65809	Human STA
5	861	100.0	4839	11	ADP65729	Human tra
6	861	100.0	4839	12	ADM67045	Human hom
7	861	100.0	4839	13	ADR65875	Human pro
8	861	100.0	4839	13	ADR66778	Human pro
9	861	100.0	4911	13	ACN40804	Human pro
10	810	94.1	1383	10	ADC37326	Nuclear f
11	752	87.3	759	10	ADF17545	Human and
12	752	87.3	759	10	ADH62277	Human PME
13	752	87.3	759	12	ADO39827	Human PME
14	752	87.3	1140	6	AEK92120	Prostate
15	752	87.3	1140	10	ADG60105	Human and
16	752	87.3	1140	10	ADH62276	Human PME
17	752	87.3	1140	12	ADO39826	Human PME
18	752	87.3	1141	10	ADB75588	Prostate
19	752	87.3	1850	8	ACC49536	Tumour-as
20	752	87.3	4527	11	ADL83313	Human and

Qy	661	GGCGGCGGGCGGATGAGAGGGGCGCGCCCACTTAAGGAGAGTCAATGGCCACTACCGG	720
Db	981	AGCGGCGGGCGATGAGAGGGGCGCGCCCACTTAAGGAGAGTCAATGGCCACTACCGG	104
Qy	721	GGGTCCTCCCTTCAGACACGAGAGCAATGGGCGCCCTCTCTGTGTGAGGGGACCCGG	780
Db	1041	GGGTCCTCTCTTCACGACCAAGAGAGCAATGGGCGCCCTCTCTGTGTGAGGGGACCCGG	110
Qy	781	CTCCACCAACACACATCGCGCCCTTAGAGAGCGACGCAATCTGAGCAAAAGAGAGAT	840
Db	1101	CTCCACCAACACACATCGCGCCCTTAGAGAGCGACGCAATCTGAGCAAAAGAGAGAT	116
Qy	841	AAACAGAAAGGACACCCCTCTC	861
Db	1161	AAACAGAAAGGACACCCCTCTC	1181
RESULT 7			
ADRe5875			
ID	ADRe5875 standard; DNA; 4839 BP.		
XX	ADRe5875;		
XX	02-DEC-2004 (first entry)		
XX	Human prostatic carcinoma derived DNA SEQ ID 71 #1.		
XX	human; cytostatic; diagnosis; prostatic cancer;		
KW	differential expression analysis; ds.		
XX	Homo sapiens.		
XX	WO2004076614-A2.		
XX	10-SEP-2004.		
PD	22-FEB-2004; 2004WO-DE000433.		
PF	27-FEB-2003; 2003DE-01009985.		
PR	14-MAY-2003; 2003DE-01022134.		
XX	(HINZ/) HINZMANN B.		
PA	(DAHL/) DAHL E.		
PA	(ROSE/) ROSENTHAL A.		
PA	(HERM/) HERMANN K.		
XX	(PIL/) PILARSKY C.		
P1	Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T,		
P1	Schmitz A, Beckmann G, Brummendorf T, Kluememann H, Reepke S;		
P1	Xinzhong L, Staud E,		
XX	WPI; 2004-653386/63.		
XX	New nucleic acids, and encoded proteins, from prostatic cancer tissue,		
PT	useful for diagnosis, treatment and in screening for specific binding		
PT	agents.		
XX	Claim 1, Page 277; 1607pp; German.		
CC	This invention describes novel cytostatic polynucleotide and polypeptide		
CC	sequences which can be used in a method for diagnosing prostatic cancer		
CC	or the risk of developing prostatic cancer. Diagnosis is based on		
CC	determining over transcription or over expression of the sequences in		
CC	prostatic tissue. Screening for inhibitors of the sequences or detection		
CC	substances involves a binding assay, any compounds that bind are		
CC	selected, optionally after deconvolution of mixtures. Detection of a		
CC	predetermined minimum level of the reporter indicates the presence of		
CC	tumour cells. Inhibitors can be chosen from antisense oligonucleotides,		
CC	thumt-interfering RNA or ribozymes; an organic molecule of molecular		
CC	weight below 5000, preferably 300, that binds to the polypeptide; an		
CC	aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the		
CC	polypeptide, preferably humanised or human; an anti-idiotypic, non-human		

[illegible]

Qy 841 AAACGAAAGACACCTCTC 861
 Db 1161 AAACGAAAGACACCTCTC 1181

RESULT 9

ACN40804
 ID ACN40804 standard; cDNA; 4911 BP.

ACN40804;

18-NOV-2004 (first entry)

Tumour-associated antigenic target (TAT) cDNA DNA326860, SEQ ID NO:5823.

Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 tumour; diagnosis; cell proliferative disorder; breast cancer;
 colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 central nervous system cancer; bladder cancer; pancreatic cancer;
 cervical cancer; melanoma; leukaemia; hybridisation probe;
 chromosome identification; chromosome mapping; gene mapping;
 gene therapy; cytoabatic; gene; ss.

Homo sapiens.

WO2004030615-A2.

15-APR-2004.

29-SEP-2003; 2003WO-US028547.

02-OCT-2002; 2002US-0414971P.

(SETH) GENENTECH INC.

Wu TD, Zhang Z, Zhou Y;

WPI; 2004-347921/32.

New tumor-associated antigenic target polypeptides and nucleic acids,
 useful in preparing a medicament for treating or detecting a
 proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 prostate cancer or tumor.

Claim 1; SEQ ID NO 5823; 7273bp; English.

The invention relates to human tumour-associated antigenic target (TAT)
 polypeptides, and their related nucleic acids. The TAT polypeptides are
 overexpressed in cancer tissues compared to normal tissues, and may thus
 serve as effective targets for the diagnosis and treatment of cancer in
 mammals. The invention also relates to nucleic acid and polypeptide
 sequences at least 80% identical to the TAT nucleic acids and
 polypeptides; expression vectors and host cells comprising a TAT nucleic
 acid; an antibody specific for a TAT polypeptide; a peptide or organic
 molecule which binds to a TAT polypeptide; fusion proteins comprising a
 TAT polypeptide; and methods and compositions for the treatment or
 diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 antibodies, antagonists, binding molecules and compositions are useful
 for diagnosing or treating a cell proliferative disorder associated with
 increased TAT expression, particularly cancers such as breast cancer,
 colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 cancer, pancreatic cancer, cervical cancer, cancers of the central
 nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 used as hybridisation probes, in chromosome and gene mapping, in
 chromosome identification and in gene therapy. The present sequence
 represents a TAT nucleic acid of the invention

Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;

Query Match 100.0%; Score 861; DB 13; Length 4911;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACCCGCTTGAATGAGGAGTCAACAGACCGCCGCGCGCGGAGCCCAATGTC 60
 Db 393 ATGACCCGCTTGAATGAGGAGTCAACAGACCGCCGCGCGCGGAGCCCAATGTC 452
 Qy 61 TCCTGACAGTGAACATGCAAAAGCTCTTTGTTCCAGACATGAGATCAAGAGCTGAG 120
 Db 453 TCCTGACAGTGAACATGCAAAAGCTCTTTGTTCCAGACATGAGATCAAGAGCTGAG 512
 Qy 121 TTTGTTGAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 180
 Db 513 TTTGTTGAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 572
 Qy 181 CTGCTGAGCACTCAAGCTGTCTGACAGGCTCTTCAATCAGCCGCGCAGCCAGGCGG 240
 Db 573 CTGCTGAGCACTCAAGCTGTCTGACAGGCTCTTCAATCAGCCGCGCAGCCAGGCGG 632
 Qy 241 AGAGAGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 Db 633 AGAGAGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 Qy 301 GGCAGCGGAATCCAGAGCCGCGAGCTTACGCCCCGCTGCGCCAGCCAGCCGCTGCG 360
 Db 693 GGCAGCGGAATCCAGAGCCGCGAGCTTACGCCCCGCTGCGCCAGCCAGCCGCTGCG 752
 Qy 361 GTGCGCCCTTGGCCGAGCGGAGCGCTTCAACCGCTTCCAGCCCACTTACCTG 420
 Db 753 GTGCGCCCTTGGCCGAGCGGAGCGCTTCAACCGCTTCCAGCCCACTTACCTG 812
 Qy 421 CAGCAGAGATGACCTGTCACCCACCATCTGCTGTCAGACGGGAGAGAGAGAGAGAG 480
 Db 813 CAGCAGAGATGACCTGTCACCCACCATCTGCTGTCAGACGGGAGAGAGAGAGAGAG 872
 Qy 481 TACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 Db 873 TACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 932
 Qy 541 GAGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 Db 933 GAGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 992
 Qy 601 AGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 Db 993 AGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1052
 Qy 661 AGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 Db 1053 AGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1112
 Qy 721 GGGTCCTCTTCCAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 Db 1113 GGGTCCTCTTCCAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1172
 Qy 781 CTCACACACACACATCGGCGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 Db 1173 CTCACACACACACATCGGCGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1232
 Qy 841 AAACGAAAGACACCTCTC 861
 Db 1233 AAACGAAAGACACCTCTC 1253

RESULT 10

AD37326
 ID AD37326 standard; DNA; 1383 BP.

AD37326;

18-DEC-2003 (first entry)

Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 159.

Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;

Accession	Sequence	Position
Db	545 CTTGCTACCGCAGCGCGGCGCATGAGGGGCGCGCCACCTACAGCGAGGTCATCG	604
Oy	710 GCCACTACCCGGGGGTCTCTCTTCACAGCACCAGAGAGCAGTGGGCGCCCTCTCTGCTGG	769
Db	605 GGCACCTACCCGGGGGTCTCTCTTCAGAGCACCAGAGAGCATGGGAGCGCCCTCTTGCTGG	664
Oy	770 AGGGGACCCGGGCTCCACCAACAACATCGCGCCCTTAGAGAGCGCAGCCATCTGGACA	829
Db	665 AGGGGACCCGGGCTCCACCAACAACAATCGCGCCCTTAGAGAGCGCAGCATCTGGACA	724
Oy	830 AAGAGAGGATAAACGAAAGGACACCTCTTC	861
Db	725 AAGAGAGGATAAACGAAAGGACACCTCTTC	756

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 18:46:54 ; Search time 159.021 Seconds
(without alignments)
8859.444 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861
Sequence: 1 atgcacccctgatg999gtc.....aacagaagacacccctc 861

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 81813359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	87.3	759	US-09-769-482-2	Sequence 2, Appli
2	752	87.3	1140	US-09-769-482-1	Sequence 1, Appli
3	30	3.5	142783	US-09-949-016-15127	Sequence 15127, A
4	29	3.4	3430	US-09-949-016-1263	Sequence 1263, Ap
5	29	3.4	9406	US-09-949-016-13005	Sequence 13005, A
6	29	3.4	34230	US-09-949-016-12052	Sequence 12052, A
7	29	3.4	128470	US-09-949-016-13765	Sequence 13765, A
8	26	3.0	198942	US-09-949-016-13209	Sequence 13209, A
9	26	3.0	254405	US-09-949-016-14381	Sequence 14381, A
10	24	2.8	431	US-09-513-9999C-9263	Sequence 9263, Ap
11	24	2.8	119762	US-09-949-016-17313	Sequence 17313, A
12	23	2.7	377	US-08-332-766A-1	Sequence 1, Appli
13	23	2.7	1212	US-09-248-796A-6566	Sequence 6566, Ap
14	23	2.7	10304	US-09-627-465B-1	Sequence 1, Appli
15	23	2.7	55195	US-09-949-016-15854	Sequence 15854, A
16	22	2.6	22	US-09-769-482-8	Sequence 8, Appli
17	22	2.6	209	US-09-513-9999C-14394	Sequence 14394, A
18	22	2.6	39154	US-09-949-016-12384	Sequence 12384, A
19	22	2.6	39154	US-09-949-016-12801	Sequence 12801, A
20	22	2.6	39443	US-09-949-016-14326	Sequence 14326, A
21	22	2.6	39443	US-09-949-016-14327	Sequence 14327, A
22	22	2.6	70770	US-09-949-016-16938	Sequence 16938, A
23	22	2.6	94019	US-09-949-016-13203	Sequence 13203, A
24	22	2.4	633	US-08-234-783-1	Sequence 1, Appli
25	21	2.4	633	US-08-456-907-1	Sequence 1, Appli
26	21	2.4	633	PCT-US95-05523-1	Sequence 1, Appli
27	21	2.4	1327	US-08-165-315D-3	Sequence 3, Appli

28	21	2.4	1661	US-09-436-521A-1	Sequence 1, Appli
29	21	2.4	4659	US-08-264-578-10	Sequence 10, Appli
30	21	2.4	4659	US-08-217-704C-9	Sequence 9, Appli
31	21	2.4	4659	US-08-164-487A-1	Sequence 1, Appli
32	21	2.4	7710	US-09-949-016-738	Sequence 738, App
33	21	2.4	8147	US-09-514-247A-9	Sequence 9, Appli
34	21	2.4	8242	US-09-949-016-4620	Sequence 4620, Ap
35	21	2.4	8252	US-08-046-585-15	Sequence 15, Appli
36	21	2.4	8252	US-08-393-703-15	Sequence 15, Appli
37	21	2.4	8252	PCT-US93-11721-15	Sequence 15, Appli
38	21	2.4	21170	US-09-949-016-12460	Sequence 12460, A
39	21	2.4	27630	US-09-949-016-16362	Sequence 16362, A
40	21	2.4	31391	US-09-949-016-14319	Sequence 14319, A
41	21	2.4	1664976	US-08-916-421B-1	Sequence 1, Appli
42	21	2.4	1664976	US-09-692-570-1	Sequence 1, Appli
43	20	2.3	50	US-09-769-482-9	Sequence 9, Appli
44	20	2.3	50	US-08-753-247-22	Sequence 22, Appli
45	20	2.3	51	US-08-753-247-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1
US-09-769-482-2
; Sequence 2, Application US/09769482

; Patent No. 6566130

; GENERAL INFORMATION:

; APPLICANT: SRIVASTAVA, SHIV

; APPLICANT: MOUL, JUDD W.

; APPLICANT: XU, LINDA L.

; APPLICANT: SEGAWA, TAKEHIKO

; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

; FILE REFERENCE: 04995, 0057-00000

; CURRENT APPLICATION NUMBER: US/09/769,482

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/178,772

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/179,045

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 759

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-769-482-2

Query Match 87.3%; Score 752; DB 4; Length 759;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	110	CGAGCTGAGGTTGTCAGATCATCATCATCTGTGTGATGATGATGATGATGATG	169
DB	5	CGAGCTGAGGTTGTCAGATCATCATCATCTGTGTGATGATGATGATGATGATG	64
QY	170	TGATCATGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG	229
DB	65	TGATCATGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG	124
QY	230	GCCAGGGGGGAGAGAGAGATGCTGCTGCTGATGATGATGATGATGATGATG	289
DB	125	GCCAGGGGGGAGAGAGATGCTGCTGCTGATGATGATGATGATGATGATGATG	184
QY	290	GCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	349
DB	185	GCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	244
QY	350	ACCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	409
DB	245	ACCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	304

Qy 410 ATCCGTACCTGAGCAGAGATGACCTGCAACCCACCATCTGCTGTCAAGCGGGAGG 469
Db 305 ATCCGTACCTGAGCAGAGATGACCTGCAACCCACCATCTGCTGTCAAGCGGGAGG 364
Qy 470 AGCCCCCCTTACCAAGGAGCCCTTGAACCTTCAAGCTTGGGAGCCCGAGCAGAGCTGG 529
Db 365 AGCCCCCCTTACCAAGGAGCCCTTGAACCTTCAAGCTTGGGAGCCCGAGCAGAGCTGG 424
Qy 530 AACTGAACCGGAGTCTGAGCGCGCAGCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGA 589
Db 425 AACTGAACCGGAGTCTGAGCGCGCAGCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGA 484
Qy 590 TGGATAGTGCAGAGCTGAGCGCGCAGCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGA 649
Db 485 TGGATAGTGCAGAGCTGAGCGCGCAGCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGA 544
Qy 650 CGTGTACGAGCAGCG 709
Db 545 CGTGTACGAGCAGCG 604
Qy 710 GCCACTACCCGGGGTCTCTCTCCAGCAGCAGAGAGAGTGGCGCGCGCTCTTGTCTGG 769
Db 605 GCCACTACCCGGGGTCTCTCTCCAGCAGCAGAGAGAGTGGCGCGCGCTCTTGTCTGG 664
Qy 770 AGGGGACCCGGCTCCACACACACATCGCGCCCTTGAAGAGCGGACCATCTTGAAGCA 829
Db 665 AGGGGACCCGGCTCCACACACACATCGCGCCCTTGAAGAGCGGACCATCTTGAAGCA 724
Qy 830 AAGGAAGATTAACAGAAAGACACCTCTTC 861
Db 725 AAGGAAGATTAACAGAAAGACACCTCTTC 756

RESULT 2

US-09-769-482-1
; Sequence 1, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOULI, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995, 0057-0000
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US/09/769, 482
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/1178, 772
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(850)
US-09-769-482-1

Query Match 87.3%; Score 752; DB 4; Length 1140;

Best Local Similarity 100.0%; Pred, No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 CGAGGCTGAGTGTTCATATCATATCGTGGTGGATGATGATGATGATGATGATGATGATGATG 169
Db 99 CGAGGCTGAGTGTTCATATCATATCGTGGTGGATGATGATGATGATGATGATGATGATGATG 158
Qy 170 TGAATCAGTCTGCTGAGCAGCTAAGAGTGTCTGAGCGGCTCTTATCATGAGCGGAGCA 229
Db 159 TGAATCAGTCTGCTGAGCAGCTAAGAGTGTCTGAGCGGCTCTTATCATGAGCGGAGCA 218

Qy 230 GCCAGGGGCGAGGAGAGATGCGCTGTCTCAGAGAGATGCGTGGCCCTCGGAGA 289
Db 219 GCCAGGGGCGAGGAGAGATGCGCTGTCTCAGAGAGATGCGTGGCCCTCGGAGA 278
Qy 290 GCACAGTGTGAGGAGAGATGCGAGAGCGGAGAGTCTAAGCGCCCGCTCGGAGCAAG 349
Db 279 GCACAGTGTGAGGAGAGATGCGAGAGCGGAGAGTCTAAGCGCCCGCTCGGAGCAAG 338
Qy 350 ACCGCTGAGCGTGGCGCCCTTGGCCGAGGAGCGCTTTCAGCGCTTCCAGCCCACT 409
Db 339 ACCGCTGAGCGTGGCGCCCTTGGCCGAGGAGCGCTTTCAGCGCTTCCAGCCCACT 398
Qy 410 ATCCGTACCTGAGCAGAGATGAGCTGCAACCCACCATCTGCTGTGAGAGGAGG 469
Db 399 ATCCGTACCTGAGCAGAGATGAGCTGCAACCCACCATCTGCTGTGAGAGGAGG 458
Qy 470 AGCCCCCCTTACCAAGGAGCCCTTGAACCTTCAAGCTTGGGAGCCCGAGCAGAGCTGG 539
Db 459 AGCCCCCCTTACCAAGGAGCCCTTGAACCTTCAAGCTTGGGAGCCCGAGCAGAGCTGG 518
Qy 530 AACTGAACCGGAGTCTGAGCGCGCAGCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGA 589
Db 519 AACTGAACCGGAGTCTGAGCGCGCAGCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGA 578
Qy 590 TGGATAGTGCAGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 649
Db 579 TGGATAGTGCAGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 638
Qy 650 CGTGTACGAGCAGCG 709
Db 639 CGTGTACGAGCAGCG 698
Qy 710 GCCACTACCCGGGGTCTCTCTCCAGCAGCAGAGAGAGTGGCGCGCGCTCTTGTCTGG 769
Db 699 GCCACTACCCGGGGTCTCTCTCCAGCAGCAGAGAGAGTGGCGCGCGCTCTTGTCTGG 758
Qy 770 AGGGGACCCGGCTCCACACACACATCGCGCCCTTGAAGAGCGGACCATCTTGAAGCA 829
Db 759 AGGGGACCCGGCTCCACACACACATCGCGCCCTTGAAGAGCGGACCATCTTGAAGCA 818
Qy 830 AAGGAAGATTAACAGAAAGACACCTCTTC 861
Db 819 AAGGAAGATTAACAGAAAGACACCTCTTC 850

RESULT 3

US-09-949-016-15127
; Sequence 15127, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15127
; LENGTH: 142783
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(142783)
; OTHER INFORMATION: n = A, T, C, or G

RESULT 8

US-09-949-016-13209/C
; Sequence 13209, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13209
; LENGTH: 198942
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(198942)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13209

Query Match

Best Local Similarity 3.0%; Score 26; DB 4; Length 198942;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TGGTGTGATGATGATGATGATGATGATG 171

DB 42279 TGGTGTGATGATGATGATGATGATGATG 42254

RESULT 9

US-09-949-016-14381/C
; Sequence 14381, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14381
; LENGTH: 254405
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14381

Query Match

Best Local Similarity 3.0%; Score 26; DB 4; Length 254405;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TGGTGTGATGATGATGATGATGATGATG 171

DB 214182 TGGTGTGATGATGATGATGATGATGATG 214157

RESULT 10

US-09-513-999C-9263
; Sequence 9263, Application US/0951399C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ductert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 9263
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-9263

Query Match

Best Local Similarity 2.8%; Score 24; DB 4; Length 431;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 GATGATGATGATGATGATGATGATGATG 173

DB 192 GATGATGATGATGATGATGATGATGATG 215

RESULT 11

US-09-949-016-17313
; Sequence 17313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17313
; LENGTH: 119762
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17313

Query Match

Best Local Similarity 2.8%; Score 24; DB 4; Length 119762;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GTGTGTGATGATGATGATGATGATGATG 165

DB 61518 GTGTGTGATGATGATGATGATGATGATG 61541

RESULT 12

US-08-332-766A-1
; Sequence 1, Application US/08332766A
; Patent No. 5843647
; GENERAL INFORMATION:
; APPLICANT: JEFFREYS, Alec J.
; APPLICANT: ARMOUR, John

TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
US-08-332-766A-1

Query Match 2.7%; Score 23; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGTGTGATGATGATGATG 165
DB 123 TGGTGTGATGATGATGATG 145

RESULT 13
US-09-248-796A-6566/C
Sequence 6566, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6566
LENGTH: 1212
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-6566

Query Match 2.7%; Score 23; DB 4; Length 1212;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GTGGTGTGATGATGATGATG 164
DB 342 GTGGTGTGATGATGATGATG 320

RESULT 14
US-09-627-465B-1
Sequence 1, Application US/09627465B
Patent No. 6737519
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
APPLICANT: LITTLE, RANDALL D.
APPLICANT: BERGEWEGH, PAUL VAN
APPLICANT: DUPUIS, JOSEF
APPLICANT: DEL MASTRO, RICHARD L.
APPLICANT: SIMON, JASON
APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NOVEL HUMAN GENES RELATING TO RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4037
CURRENT APPLICATION NUMBER: US/09/627,465B
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/146,336
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentn Ver 2.1
SEQ ID NO 1
LENGTH: 10304
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (267)
OTHER INFORMATION: a, t, c or g
US-09-627-465B-1

Query Match 2.7%; Score 23; DB 4; Length 10304;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGTGTGATGATGATGATG 165
DB 10242 TGGTGTGATGATGATGATG 10264

RESULT 15
US-09-949-016-15854/C
Sequence 15854, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15854
LENGTH: 55195
TYPE: DNA
ORGANISM: Human
US-09-949-016-15854

Query Match 2.7%; Score 23; DB 4; Length 55195;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 19:27:04 ; Search time 483.77 Seconds
(without alignments)
10519.334 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcaccgcctgctgagggggtc.....aacagaagacaccccttc 861

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5384158 seqs, 2955248155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	861	100.0	861	9	US-09-934-249-3
2	861	100.0	864	17	US-10-295-027-127
3	861	100.0	1321	9	US-09-934-249-1
4	861	100.0	4839	15	US-10-241-220-119
5	861	100.0	4839	16	US-10-269-909-84
6	861	100.0	4839	16	US-10-269-909-85
7	861	100.0	4839	18	US-10-872-972-119
8	861	100.0	4839	18	US-10-872-972-119
9	752	87.3	759	16	US-10-390-045-2
10	752	87.3	759	17	US-10-434-479-2
11	752	87.3	1140	16	US-10-390-045-1

12	752	87.3	1140	17	US-10-434-479-1	Sequence 1, Appl1
13	752	87.3	1141	15	US-10-205-823-412	Sequence 412, App
14	752	87.3	1141	15	US-10-301-822-208	Sequence 208, App
15	752	87.3	1850	15	US-10-241-220-44	Sequence 44, Appl
16	752	87.3	1850	18	US-10-872-972-44	Sequence 44, Appl
17	752	87.3	1850	18	US-10-872-972-44	Sequence 44, Appl
18	752	87.3	4527	18	US-09-821-812-2	Sequence 2, Appl1
19	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
20	740	85.9	1066	13	US-10-098-841-71	Sequence 71, Appl
21	701	81.4	806	15	US-10-241-220-45	Sequence 45, Appl
22	701	81.4	806	18	US-10-872-972-45	Sequence 45, Appl
23	701	81.4	806	18	US-10-872-972-45	Sequence 45, Appl
24	701	81.4	806	10	US-09-796-753-55	Sequence 55, Appl
25	544	63.2	1583	14	US-10-000-2564-32	Sequence 32, Appl
26	302	35.1	693	9	US-09-934-249-14	Sequence 14, Appl
27	130	15.1	467	10	US-09-918-995-2074	Sequence 2074, Ap
28	102	11.8	368	9	US-09-783-590-3464	Sequence 3464, Ap
29	50	5.8	65	9	US-09-783-590-3464	Sequence 3468, Ap
30	49	5.7	60	10	US-09-908-975-13620	Sequence 13620, A
31	44	5.1	878	9	US-09-934-249-12	Sequence 12, Appl
32	44	5.1	1713	10	US-09-796-753-57	Sequence 57, Appl
33	41	4.8	475	9	US-10-240-425-166	Sequence 166, App
34	40	4.6	522	17	US-09-864-761-20542	Sequence 20542, A
35	32	3.7	577	9	US-09-864-761-20542	Sequence 376, Ap
36	32	3.7	1964	9	US-09-864-761-20542	Sequence 336, Ap
37	29	3.4	401	9	US-09-864-761-20542	Sequence 20699, A
38	29	3.4	446	9	US-09-864-761-20699	Sequence 16, Appl
39	29	3.4	3444	16	US-10-293-582-16	Sequence 108, App
40	28	3.3	30611	18	US-10-367-094-108	Sequence 250, App
41	27	3.1	51	17	US-10-418-182-250	Sequence 25133, A
42	26	3.0	1493	16	US-10-029-386-25133	Sequence 159, App
43	26	3.0	7733	9	US-09-860-670-159	Sequence 159, App
44	26	3.0	7733	17	US-10-327-646-159	Sequence 3, Appl1
45	26	3.0	8429	9	US-09-738-885-3	

ALIGNMENTS

RESULT 1
US-09-934-249-3 Application US/09934249
Sequence 3, Appl1
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turti, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 861
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(861)
US-09-934-249-3

Query Match 100.0%; Score 861; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGCACCGCTGATGAGGGGTCAACAGCAGCCGCGCGCGCGGAGCCCATGTC 60
|||||

[illegible]

```

1  APPLICANT: Eos Biotechnology, Inc.
2  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
3  TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
4  FILE REFERENCE: 018501-012500US
5  CURRENT APPLICATION NUMBER: US/10/295,027
6  CURRENT FILING DATE: 2002-11-13
7  PRIOR APPLICATION NUMBER: US 09/663,733
8  PRIOR FILING DATE: 2000-09-15
9  PRIOR APPLICATION NUMBER: US 60/350,666
10 PRIOR FILING DATE: 2001-11-13
11 PRIOR APPLICATION NUMBER: US 60/335,394
12 PRIOR FILING DATE: 2001-11-15
13 PRIOR APPLICATION NUMBER: US 60/332,464
14 PRIOR FILING DATE: 2001-11-21
15 PRIOR APPLICATION NUMBER: US 60/334,393
16 PRIOR FILING DATE: 2001-11-29
17 PRIOR APPLICATION NUMBER: US 60/340,376
18 PRIOR FILING DATE: 2001-12-14
19 PRIOR APPLICATION NUMBER: US 60/347,211
20 PRIOR FILING DATE: 2002-01-08
21 PRIOR APPLICATION NUMBER: US 60/347,349
22 PRIOR FILING DATE: 2002-01-10
23 PRIOR APPLICATION NUMBER: US 60/355,250
24 PRIOR FILING DATE: 2002-02-08
25 PRIOR APPLICATION NUMBER: US 60/356,714
26 PRIOR FILING DATE: 2002-02-13
27 Remaining Prior Application data removed - See File Wrapper or PALM.
28 NUMBER OF SEQ ID NOS: 1386
29 SOFTWARE: PatentIn Ver. 2.1
30 SEQ ID NO 127
31 LENGTH: 864
32 TYPE: DNA
33 ORGANISM: Homo sapiens
34 US-10-295-027-127

```

Query Match	100.0%	Score 861	DB 17	Length 864
Best Local Similarity	100.0%	Pred. No. 0		
Matches 861	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATGCACCGCTTGATGAGGAGTCAACAGCACCGCGCGCGCGCGCGCGAGGCCCAATATC	60	
Db	1	ATGCACCGCTTGATGAGGAGTCAACAGCACCGCGCGCGCGCGCGAGGCCCAATATC	60	
QY	61	TCCGTCAAGTGAACATGCGAAACGCTCTTTGTTCAGAGCATGAGATACGAGCTGAG	120	
Db	61	TCCGTCAAGTGAACATGCGAAACGCTCTTTGTTCAGAGCATGAGATACGAGCTGAG	120	
QY	121	TTTGTTCAGATCATCATCGTGGTGTGTATGATAGTATGTGTGTGTATCAACGAGC	180	
Db	121	TTTGTTCAGATCATCATCGTGGTGTGTATGATAGTATGTGTGTGTATCAACGAGC	180	
QY	181	CTGCTGACCCCTACAAAGCTGTCTGCAAGGTCTTTCATCAGCCGAGCAAGCCAGAGGCGG	240	
Db	181	CTGCTGACCCCTACAAAGCTGTCTGCAAGGTCTTTCATCAGCCGAGCAAGCCAGAGGCGG	240	
QY	241	AGGAGAGAAGATGCGCTGTCTCTCAGAGAAGATGCGTGTGGCCCTGTGGAGAGACAGTGTCA	300	
Db	241	AGGAGAGAAGATGCGCTGTCTCTCAGAGAAGATGCGTGTGGCCCTGTGGAGAGACAGTGTCA	300	
QY	301	GCGAACGGAATCCCAAGACCGCAGGTCTACGCGCCCGCCTCGGCCACCGACCGCCTTGACC	360	
Db	301	GCGAACGGAATCCCAAGACCGCAGGTCTACGCGCCCGCCTCGGCCACCGACCGCCTTGACC	360	
QY	361	GTGCGCGCCCTTGCGCCAGCGGAGCGGCTTTCACCGCTTTCAGAGCCCACTTATCCGTACTGTG	420	
Db	361	GTGCGCGCCCTTGCGCCAGCGGAGCGGCTTTCACCGCTTTCAGAGCCCACTTATCCGTACTGTG	420	
QY	421	CAGCAGCAGATTCGACTGTGCACCAACCATCTCGCTGTCAACGAGGAGAGAGCCCAACCC	480	
Db	421	CAGCAGCAGATTCGACTGTGCACCAACCATCTCGCTGTCAACGAGGAGAGAGCCCAACCC	480	
QY	481	TACCAAGGCCCCCGACCCCTTCAGCTTCGGGACCCCGAGCAGCACTGTGAATCGG	540	

Db	481	AACGAGGGGCGCCTGCACCTCCAGCTTCGGGAGCCCCGAGGACGAGCTGGAACTGAACCGG	540
Qy	541	GAGTCGGTGTGCGGCGCACCCCCCAACAGAACCATTTTGACAGTGAAGCTGATGGATAGTGGC	600
Db	541	GAGTCGGTGTGCGGCGCACCCCCCAACAGAACCATTTTGACAGTGAAGCTGATGGATAGTGGC	600
Qy	601	AGGCTGGGGGGGGCGCCCGCCCCCGACAGCACTAACCTGGGGCATTCAGGGCCACCTGTCTACCGC	660
Db	601	AGGCTGGGGGGGGCGCCCGCCCCCGACAGCACTAACCTGGGGCATTCAGGGCCACCTGTCTACCGC	660
Qy	661	AGCGGCGGGCGCATGTGAGGGGCGCGCCCACTTACAGCGAGGTCACTGGCCACTACCGG	720
Db	661	AGCGGCGGGCGCATGTGAGGGGCGCGCCCACTTACAGCGAGGTCACTGGCCACTACCGG	720
Qy	721	GGGTCTCTCTTCACGACACGACGAGCAGTGTGGGCGCCCTCTTGTGTGAGGGGAGCCCGG	780
Db	721	GGGTCTCTCTTCACGACACGACGAGCAGTGTGGGCGCCCTCTTGTGTGAGGGGAGCCCGG	780
Qy	781	CTTCACACACACACACATCGCGCCCTTACAGAGGCGGACCATCTGAGAGCAAAAGAAAGGAT	840
Db	781	CTTCACACACACACACATCGCGCCCTTACAGAGGCGGACCATCTGAGAGCAAAAGAAAGGAT	840
Qy	841	AAACAGAAAGACACCCCTCTC	861
Db	841	AAACAGAAAGACACCCCTCTC	861

[illegible]

Db	593	CTGCTGAGCGCACTAACAAGTGTCTGCAGCGTCTCTTCATAGCCGGCAGCCAGCGGGGCGG	652
QY	241	AGGAGAGAAAGATGCCCTGTCTCTCAGAAAGATATCCCTGTGGCCCTTCGGAGAGCAAGTGTCA	300
Db	653	AGGAGAGAAAGATGCCCTGTCTCTCAGAAAGATATCCCTGTGGCCCTTCGGAGAGCAAGTGTCA	712
QY	301	GCGCAACGGAATCCAGAGCCGCAAGGTCTTACGCGCCGCTCGGCCCAACGACGCGCTGGCC	360
Db	713	GCGCAACGGAATCCAGAGCCGCAAGGTCTTACGCGCCGCTCGGCCCAACGACGCGCTGGCC	772
QY	361	GTGCGCGCCCTTCGCCCCAGCGGGAGCGCTTTCACCGCTTTCAGCCCACTTATCCGTACTGG	420
Db	773	GTGCGCGCCCTTCGCCCCAGCGGGAGCGCTTTCACCGCTTTCAGCCCACTTATCCGTACTGG	832
QY	421	CAGCAGAGATGACCTGCGCAACCCACATCTGCTGTACAGACGGGGAGGAGCCCCACCC	480
Db	833	CAGCAGAGATGACCTGCGCAACCCACATCTGCTGTACAGACGGGGAGGAGCCCCACCC	892
QY	481	TACCAAGGAGCCCTTGACCCCTTCAGCTTTCGGGACCCCGAGCAGAGCTGGAACTGAAACCG	540
Db	893	TACCAAGGAGCCCTTGACCCCTTCAGCTTTCGGGACCCCGAGCAGAGCTGGAACTGAAACCG	952
QY	541	GAGTGTGTGTGCGCGACCCCCCAAAGAAACATCTTCGACAGTGAACCTGATGATAGTATGTGC	600
Db	953	GAGTGTGTGTGCGCGACCCCCCAAAGAAACATCTTCGACAGTGAACCTGATGATAGTATGTGC	101
QY	601	AGGCTGGAGCGGCCCTTGCCCCCCCCCAGCAGTAACTCGGGCATAGCGCCACGTCCTACCGC	660
Db	1013	AGGCTGGAGCGGCCCTTGCCCCCCCCCAGCAGTAACTCGGGCATAGCGCGCAGTGTCTACCGC	107
QY	661	AGCGGCGGGCGCATGAGAGGGGCGCGCGCCCACTTACAGGAGAGTCAATCGGCCACTTACCG	720
Db	1073	AGCGGCGGGCGCATGAGAGGGGCGCGCGCCCACTTACAGGAGAGTCAATCGGCCACTTACCG	113
QY	721	GGGTCTCTCTTCACACACAGCAGAGAGTGGGCGGCCCTCTTGTGTGAGGGGAGACCCGG	780
Db	1133	GGGTCTCTCTTCACACACAGCAGAGAGTGGGCGGCCCTCTTGTGTGAGGGGAGACCCGG	119
QY	781	CTCCACACACACACATGCGCGCCCTTAGAGAGCGAGCCATCTGAGCAAAAGAAAGAT	840
Db	1193	CTCCACACACACACATGCGCGCCCTTAGAGAGCGAGCCATCTGAGCAAAAGAAAGAT	125
QY	841	AAACGAAAGGACACCCCTCTC	861
Db	1253	AAACGAAAGGACACCCCTCTC	1273

```

RESULT 4
US-10-241-220-119
; Sequence 119, Application US/10241220
; Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-119
Query Match          100.0%; Score 861, DB 15, Length 4839;

```


Db 1101 CTCCACCAACACATCGCCGCTTAAAGAGCGCAGCCATCTGGAGCAAGAGAGAGT 1160

Qy 841 AAACGAAAGACACCTCTC 861

Db 1161 AAACGAAAGACACCTCTC 1181

RESULT 6
ITS-10-26

```

US-10-269-909-85
Sequence 85, Application US/10269909
Publication No. US20030180747A1
GENERAL INFORMATION:
APPLICANT: HRUBAN, RALPH H.
APPLICANT: ARGENTI, PEDRAM
APPLICANT: IACOBUTTO-DONAHUE, CHRISTINE
APPLICANT: MAITRA, ANIRBAN
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
FILE REFERENCE: 58303 (71699)
CURRENT APPLICATION NUMBER: US/10/269,909
CURRENT FILING DATE: 2003-10-11
PRIOR APPLICATION NUMBER: 60/328,609
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/332,754
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 85
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo sapiens
US-10-269-909-85

```

Query Match	100.0%	Score 861;	DB 16;	Length 4839;
Best Local Similarity	100.0%;	Pred. Nc. 0;		
Matches 861; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	TTGCAACCGCCTGATGAGGGGTCAACAGACACCGCCGCGCGCGCGCGCGAGGCCAATATC	60
Db	321	ATGCACCCCTTGATGATGGGGGTCAACAGCACCGCCGCGCGCGCGCGCGAGGCCAATATC	360
QY	61	TCTGCAAGTGCACATGCACAAAGCTCTTTGTTCCAGAGCATGGAGATCAAGAGCTGGAG	120
Db	381	TCTGCAAGTGCACATGCACAAAGCTCTTTGTTCCAGAGCATGGAGATCAAGAGCTGGAG	440
QY	121	TTTGTTCAGATCATCATCATCGGTGTGTGATGATGATGATGATGATGATCAAGTGC	180
Db	441	TTTGTTCAGATCATCATCATCGGTGTGTGATGATGATGATGATGATGATGATCAAGTGC	500
QY	181	CTGCTGAGCCTACTACAGCTGTCTGTGACCGTCTTCATCAGCCGCGACAGCCAGGGGCGG	240
Db	501	CTGCTGAGCCTACTACAGCTGTCTGTGACCGTCTTCATCAGCCGCGCGACAGCCAGGGGCGG	560
QY	241	AGGAGAGAAAGTGGCCCTGTGCTCAGAAAGATGCTGTGGCCCTCGGAGAGCANAAGTGTCA	300
Db	561	AGGAGAGAAAGTGGCCCTGTGCTCAGAAAGATGCTGTGGCCCTCGGAGAGCANAAGTGTCA	620
QY	301	GGCAACGGAATCCCAAGAGCCGAGGCTTCAGCCCGGCTCGGCGCCACGAGCGGCTGGCC	360
Db	621	GGCAACGGAATCCCAAGAGCCGAGGCTTCAGCCCGGCTCGGCGCCACGAGCGGCTGGCC	680
QY	361	GTGCGCCCTTCGCCAGCGGAGGCGCTTCACACCGCTTCAGGCCCACTATCCGTACTTG	420
Db	681	GTGCGCGCTTCGCCAGCGGAGGCGCTTCACACCGCTTCAGGCCCACTATCCGTACTTG	740
QY	421	CAGCAGAGATGCACCTGCGCACCCACATCTGCTGTCAAGCGGGAGAGGCCCAACC	480
Db	741	CAGCAGAGATGCACCTGCGCACCCACATCTGCTGTCAAGCGGGAGAGGCCCAACC	800
QY	481	TACCAAGGGCCCTGCAACCTCCAGCTTGGGGACCCCGACACAGAGGTGGAACTGAACCGG	540
Db	801	TACCAAGGGCCCTGCAACCTCCAGCTTGGGGACCCCGACACAGAGGTGGAACTGAACCGG	860

OY	541	GAGTCGGTGGCGGACACCCCAAGAACCATCTTCCAGACGTGACTCTGATGGATATGCGC	600
Db	861	GAGTCGGTGGCGGACACCCCAAGAACCATCTTCCAGACGTGACTCTGATGGATATGCGC	920
OY	601	AGGCTGGGCGGCGCCCTCTGCCCCAGAGATTAATCGGGCATCAGCGCATCTGCTTACGGC	660
Db	921	AGGCTGGGCGGCGCCCTCTGCCCCAGAGATTAATCGGGCATCAGCGCATCTGCTTACGGC	980
OY	661	AGCGGCGGGCGCATGAGGGGCGCGGCCCATCTTACAGCGAGGTCAATCGCCACTTACCGG	720
Db	981	AGCGGCGGGCGCATGAGGGGCGCGGCCCATCTTACAGCGAGGTCAATCGCCACTTACCGG	1040
OY	721	GGGTCTCTCTTCCAGCACCAAGAGAGCATGTGGGCGCGCTCTTGTCTGAGAGGGGACCCCG	780
Db	1041	GGGTCTCTCTTCCAGCACCAAGAGAGCATGTGGGCGCGCTCTTGTCTGAGAGGGGACCCCG	1100
OY	781	CTCCACCAACACACATCGCGCCCTCTGAGAGCGCAGCCCATCTTGGAGCAAAAGAGAGAT	840
Db	1101	CTCCACCAACACACATCGCGCCCTCTGAGAGCGCAGCCCATCTTGGAGCAAAAGAGAGAT	1160
OY	841	AAACAGAAAGGACACCTCTTC	861
Db	1161	AAACAGAAAGGACACCTCTTC	1181

RESULT 7

```

US-10-872-972-119
Sequence 119, Application US/10872972
Publication No. US20040229277A1
GENERAL INFORMATION:
APPLICANT: Frantz,Gretchen
APPLICANT: Hillan,Kenneth J.
APPLICANT: Phillips,Heidi
APPLICANT: Polakis,Paul
APPLICANT: Spencer,Susan
APPLICANT: Williams,P. Mickey
APPLICANT: Wt,Thomas
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,972
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo Sapien
US-10-872-972-119

```

Query Match	100.0%	Score 861;	DB 18;	Length 4839;
Best Local Similarity	100.0%	Pred. No.0;		
Matches 861;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy	2	ATGCAACGGTTATATGGGGGGTCAACAGCACCGCGCGCGCGCGCGGAGACCCCAATGTC	60
Db	321	ATCACACGGCTTATATGGGGGTCAACAGCACCGCGCGCGCGCGCGGAGACCCCAATGTC	360
Qy	61	TCCTGCACGTGCACCTGCMAACGCTCTTGTTCAGAGCATGAGATCAAGAGCTGGAG	120
Db	381	TCCTGCACGTGCACCTGCMAACGCTCTTGTTCAGAGCATGAGATCAAGAGCTGGAG	440
Qy	121	TTTTGTTCAATCATCATCGTGTGGTGTATGATGGTATGGTGTGTGTATCATCGTGC	180
Db	441	TTTTGTTCAATCATCATCGTGTGGTGTATGATGGTGTGTGTGTATCATCGTGC	500
Qy	181	CTGCTAGGCACTACAAAGGTGTCTGCACGGTCTTTCATCAGCCGGGACACACAGGGGGCG	240
Db	501	CTGCTAGGCACTACAAAGGTGTCTGCACGGTCTTTCATCAGCCGGGACACACAGGGGGCG	560
Qy	241	AGGAGAAAGATGCCCTGCTCTCAGAGAGATGCCCTGTGGCCCTTCGGAGAGACAGATGTCA	300


```

Db 561 AGAGAGAAATATCCCTGCTCTGAGAAAGATGCTTGGCCCTCTGGAGAGCAAGTGTCA 620
Qy 301 GGCAACGAAATCCCAAGAGCCGCAAGTCTACGCCCCCTTGGCCCAAGCCGCTGTGGC 360
Db 621 GGCAACGAAATCCCAAGAGCCGCAAGTCTACGCCCCCTCTGGCCCAAGCCGCTGTGGC 680
Qy 361 GTGCGCCCTTCTGGCCGAGAGCCGCTTCAAGCCGCTTCAAGCCGCTATCCGTAAGTCTG 420
Db 681 GTGCGCCCTTCTGGCCGAGAGCCGCTTCAAGCCGCTTCAAGCCGCTATCCGTAAGTCTG 740
Qy 421 CAGACAGAGATGCACTGCAAGCCCAATCTGCTGTCAAGCGGAGAGAGCCCAAGCC 480
Db 741 CAGACAGAGATGCACTGCAAGCCCAATCTGCTGTCAAGCGGAGAGAGCCCAAGCC 800
Qy 481 TACCAAGAGCCCTGCAAGCCCTTCAAGCTTGGGAGCCCAAGAGAGAGAGAGAGAGAG 540
Db 801 TACCAAGAGCCCTTCAAGCTTGGGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 860
Qy 541 GAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 920
Db 861 GAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Qy 921 AGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Db 981 AGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
Qy 981 AGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
Db 1041 GGGTCTCTCTTCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100
Qy 1041 GGGTCTCTCTTCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100
Db 1101 CTCACACACACACACATGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAT 1160
Qy 841 AAACAGAAAGAGACACCTCTC 861
Db 1161 AAACAGAAAGAGACACCTCTC 1181

```

RESULT 8

```

US-10-872-991-119
; Sequence 119, Application US/10872991
; Publication No. US20040242860A1

```

GENERAL INFORMATION:

```

; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872,991
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-872-991-119

```

```

Query Match 100.0%; Score 861; DB 18; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;

```

```

Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACCGCTTGTATGGGGTCAACAGACCGCCGCGCGCGGAGAGCCATATGTC 60
Db 321 ATGCACCGCTTGTATGGGGTCAACAGACCGCCGCGCGCGGAGAGCCATATGTC 380
Qy 61 TCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 381 TCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440
Qy 121 TTTGTTAGATCATCATCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180
Db 441 TTTGTTAGATCATCATCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 500
Qy 181 CTGCTGAGCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 501 CTGCTGAGCCCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560
Qy 241 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 561 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
Qy 301 GGCAACGAAATCCCAAGAGCCGCAAGTCTACGCCCCCTTGGCCCAAGCCGCTGTGGC 360
Db 621 GGCAACGAAATCCCAAGAGCCGCAAGTCTACGCCCCCTTGGCCCAAGCCGCTGTGGC 680
Qy 361 GTGCGCCCTTCTGGCCGAGAGCCGCTTCAAGCCGCTTCAAGCCGCTATCCGTAAGTCTG 420
Db 681 GTGCGCCCTTCTGGCCGAGAGCCGCTTCAAGCCGCTTCAAGCCGCTATCCGTAAGTCTG 740
Qy 421 CAGACAGAGATGCACTGCAAGCCCAATCTGCTGTCAAGCGGAGAGAGAGAGAGAGAG 480
Db 741 CAGACAGAGATGCACTGCAAGCCCAATCTGCTGTCAAGCGGAGAGAGAGAGAGAGAG 800
Qy 481 TACCAAGAGCCCTGCAAGCCCTTCAAGCTTGGGAGCCCAAGAGAGAGAGAGAGAGAG 540
Db 801 TACCAAGAGCCCTTCAAGCTTGGGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
Qy 541 GAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 861 GAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 920
Qy 601 AGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 921 AGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Qy 661 AGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 981 AGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
Qy 721 GGGTCTCTCTTCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 1041 GGGTCTCTCTTCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100
Qy 781 CTCACACACACACACATGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAT 840
Db 1101 CTCACACACACACACATGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAT 1160
Qy 841 AAACAGAAAGAGACACCTCTC 861
Db 1161 AAACAGAAAGAGACACCTCTC 1181

```

RESULT 9

```

US-10-390-045-2
; Sequence 2, Application US/10390045
; Publication No. US20030170713A1

```

GENERAL INFORMATION:

```

; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOU, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

```



```

: TITLE OF INVENTION: POUCCLEOTYPE ARRAY
: FILE REFERENCE: 04995, 0057-00000
: CURRENT APPLICATION NUMBER: US/10/390, 045
: CURRENT FILING DATE: 2003-03-18
: PRIOR APPLICATION NUMBER: US/09/769, 482
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178, 772
: PRIOR FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/179, 045
: PRIOR FILING DATE: 2000-01-31
: NUMBER OF SEQ ID NOS: 67
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 759
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-390-045-2

```

Query Match	87.3%;	Score 752;	DB 16;	Length 759;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 752;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	110	GGAGCTGGAGTTTGTCAAGTCAATCATCATCTGTGTGGTGAATGAGTGAATGGTGAATGGTGGTGG	169
Db	5	CGAGCTGGAGTTTGTCAAGTCAATCATCATCTGTGTGGTGAATGAGTGAATGGTGAATGGTGGTGG	64
QY	170	TGATCACGTGCTGTGTGAGCCACTCAAGCTGTCTGACGGTCTCTTCATCAGCCGGACA	229
Db	65	TGATCACGTGCTGTGTGAGCCACTCAAGCTGTCTGACGGTCTCTTCATCAGCCGGACA	124
QY	230	GCCAGGGGCGGAGGAGAGAGATGCTCTGTCTTCAGAAAGATGCTGTGGCCCTTGGAGA	289
Db	125	GCCAGGGGCGGAGGAGAGAGATGCTCTGTCTTCAGAAAGATGCTGTGGCCCTTGGAGA	184
QY	290	GCAcAGTTCAGGCAACGGAAATCCGAGAGCCGAGGTCTAGCGCCCGGCTCGGACCCACCG	349
Db	185	GCAcAGTGTcAGGCAACGGAAATCCGAGAGCCGAGGTCTAGCGCCCGGCTCGGACCCACCG	244
QY	350	ACCGCTTGCGGTGCTGCGCTTTCGCCCAGCGGAGCGCTTCCACCGCTTCAGCCCACT	409
Db	245	ACCGCTTGCGGTGCTGCGCTTTCGCCCAGCGGAGCGCTTCCACCGCTTCAGCCCACT	304
QY	410	ATTCGTACTTGACAGACAGAGATGACTTGCACACCCACCATCTCGCTGTGACGCGGAGAG	469
Db	305	ATTCGTACTTGACAGACAGAGATGACTTGCACACCCACCATCTCGCTGTGACGCGGAGAG	364
QY	470	AGCCCCACCTTACCAAGGGGCCCCCTTGCACCTTCAGCTTTCGGGACCCCGAGAGAGCTGG	529
Db	365	AGCCCCACCTTACCAAGGGGCCCCCTTGCACCTTCAGCTTTCGGGACCCCGAGAGAGCTGG	424
QY	530	AACTGAACCGGGAGTTCGGTGCSCGACCCCCAAACAGAAACATCTTTCGACAGTGACTTGA	589
Db	425	AACTGAACCGGGAGTTCGGTGCSCGACCCCCAAACAGAAACATCTTTCGACAGTGACTTGA	484
QY	590	TGATATGTGCAAGGCTGGGGCGGCCCCCTTGCACCGAGTAACTCGGGCATCAGCGCCA	649
Db	485	TGATATGTGCAAGGCTGGGGCGGCCCCCTTGCACCGAGTAACTCGGGCATCAGCGCCA	544
QY	650	CGTGTCAACGACGCGCGGGGCGCATATGAGAGGGGCGCCGCCCACTACAGCGAGGTCACTG	709
Db	545	CGTGTCAACGACGCGCGGGGCGCATATGAGAGGGGCGCCGCCCACTACAGCGAGGTCACTG	604
QY	710	GCACACTACCGGGGGTCTCTCTTCAGAGCACACAGACAGACAGTGGAGCGGCTCTCTTGCTGG	769
Db	605	GCACACTACCGGGGGTCTCTCTTCAGAGCACACAGACAGACAGTGGAGCGGCTCTCTTGCTGG	664
QY	770	AGGGGACCCGGTCCACCAcACACATTCGCGCCCTTAGAGAGCGCAGGCATCTGAGACA	829
Db	665	AGGGGACCCGGTCCACCAcACACATTCGCGCCCTTAGAGAGCGCAGGCATCTGAGACA	724
QY	830	AAAGAAAGATTAACAAAGAACACCTCTTC	861
Db	725	AAAGAAAGATTAACAAAGAACACCTCTTC	756

```

: RESULT 10
: US-10-434-479-2
: Sequence 2, Application US/10434479
: Publication No. US20040092469A1
: GENERAL INFORMATION:
: APPLICANT: SRIVASTAVA, SHIV
: APPLICANT: MOUL, JUDD W.
: APPLICANT: XU, LINDA L.
: TITLE OR INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
: FILE REFERENCE: 04995.0057-02000
: CURRENT APPLICATION NUMBER: US/10/434,479
: CURRENT FILING DATE: 2003-05-09
: PRIOR APPLICATION NUMBER: 10/390,045
: PRIOR FILING DATE: 2003-03-18
: PRIOR APPLICATION NUMBER: 09/769,482
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,772
: PRIOR FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/179,045
: PRIOR FILING DATE: 2000-01-31
: NUMBER OF SEQ ID NOS: 81
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 759
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-434-479-2

```

Query Match	87.3%	Score 752;	DB 17;	Length 759;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 752; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	110	CGAGCGTGAAGTTGTTTCAGATCATCATCGTGTGTGTGTATGTATGTATCGTTGTGTG	165
Db	5	CGAGCGTGAAGTTGTTTCAGATCATCATCGTGTGTGTGTATGTATGTATCGTTGTGTG	64
OY	170	TGATCACGTGCTCTGTAGCCATCAAGAAGCTGTCTGACGGTCTTTCATCAGCCGGACACA	229
Db	65	TGATCACGTGCTCTGTAGCCATCAAGAAGCTGTCTGACGGTCTTTCATCAGCCGGACACA	124
OY	230	GCCAGGGGCGAGGAGAGAAAGATGCCCTGTCTTCAGAGAGATGCTGTGGCCTTCGAGAGA	289
Db	125	GCCAGGGGCGAGGAGAGAAAGATGCCCTGTCTTCAGAGAGATGCTGTGGCCTTCGAGAGA	184
OY	290	GCAACGTGTACGGGCAAGGAATCCCAAGCCGCAAGGTCTAAGCCCGCTTCGGCCACCG	349
Db	185	GCAACGTGTACGGGCAAGGAATCCCAAGCCGCAAGGTCTAAGCCCGCTTCGGCCACCG	244
OY	350	ACGCGCTGGGCGGTGCGGCCCTTGCGCCAGGCGGAGCGCTTCCACCGCTTCCAGGCCACCT	409
Db	245	ACGCGCTGGGCGGTGCGGCCCTTGCGCCAGGCGGAGCGCTTCCACCGCTTCCAGGCCACCT	304
OY	410	ATTCGTACTGTGACACAGATTCGACCTTGCCACCCACCATCTCGCTGTACAGCGGGAGG	469
Db	305	ATTCGTACTGTGACACAGATTCGACCTTGCCACCCACCATCTCGCTGTACAGCGGGAGG	364
OY	470	AGCCCCACCTTCACAGGGGCCCTCTGCACCTTCCAGCTTTCGGAGACCCGACGACGACTGG	529
Db	365	AGCCCCACCTTCACAGGGGCCCTCTGCACCTTCCAGCTTTCGGAGACCCGACGACGACTGG	424
OY	530	AACAGAACCGGGAAGTCGATGCGGCAACCCCAACAGAACCATCTTTCGACAGTACCTGA	589
Db	425	AACAGAACCGGGAAGTCGATGCGGCAACCCCAACAGAACCATCTTTCGACAGTACCTGA	484
OY	590	TGATTAATGCGAGGCTGGGCGGCCCTGTGCCCCCCAGCAGTAACTTCGGGCAATCAGGCCA	649
Db	485	TGATTAATGCGAGGCTGGGCGGCCCTGTGCCCCCCAGCAGTAACTTCGGGCAATCAGGCCA	544
OY	650	CGTGTCTACGGCAGGCGGGCGGCGATTCGAGGGGGCGCCGCCACCTTAAGAGAGGTCTATCG	709
Db	545	CGTGTCTACGGCAGGCGGGCGGCGATTCGAGGGGGCGCCGCCACCTTAAGAGAGGTCTATCG	604

QY 710 GCCACTACCCGGGTCCTCTTCCAGACACAGAGAGAGTGGCCGCTCTTGTCTGG 769
 Db 605 GCCACTACCCGGGTCCTCTTCCAGACACAGAGAGAGTGGCCGCTCTTGTCTGG 664
 QY 770 AGGGAGCCCGGCTCCACCAACAACATCGCGCCCTTAGAGAGCGACCATCTGAGCA 829
 Db 665 AGGGAGCCCGGCTCCACCAACAACATCGCGCCCTTAGAGAGCGACCATCTGAGCA 724
 QY 830 AAGAGAGATTAACAGAAAGAGACCCCTCTC 861
 Db 725 AAGAGAGATTAACAGAAAGAGACCCCTCTC 756

RESULT 11

US-10-390-045-1
 ; Sequence 1, Application US/10390045
 ; Publication No. US20030170713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SRIVASTAVA, SHIV
 ; APPLICANT: MOULI, JUDDA W.
 ; APPLICANT: XU, LINDA L.
 ; APPLICANT: SEGAWA, TAKEHIKO
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 ; FILE REFERENCE: 04995.0057-00000
 ; CURRENT APPLICATION NUMBER: US/10/390,045
 ; PRIOR FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US/09/769,482
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,772
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,045
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1140
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (95)..(850)
 ; US-10-390-045-1

Query Match 87.3%; Score 752; DB 16; Length 1140;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 CGGAGCTGAGATTGTTCAATCATCATCTGCTGTGATGATGATGATGATGATG 169
 Db 99 CGGAGCTGAGATTGTTCAATCATCATCTGCTGTGATGATGATGATGATGATG 158
 QY 170 TGATCAAGTGCCTGCTGACGACATCAAGCTGTCTGACGCTCTTATACGCCGACA 229
 Db 159 TGATCAAGTGCCTGCTGACGACATCAAGCTGTCTGACGCTCTTATACGCCGACA 218
 QY 230 GCCAGGGCGGAGAGAGAGATGCTCTGCTCTCAAGAGATGCTGTGCGCTCGAGA 289
 Db 219 GCCAGGGCGGAGAGAGAGATGCTCTGCTCTCAAGAGATGCTGTGCGCTCGAGA 278
 QY 290 GCACAGTGTCAAGGACGGAATCCCAAGCCGACGCTCTACGCCGCTCGGCCACCG 349
 Db 279 GCACAGTGTCAAGGACGGAATCCCAAGCCGACGCTCTACGCCGCTCGGCCACCG 338
 QY 350 ACCGCTGCGCGGCTGCGGCTCTGCGGAGAGGAGCGCTTCAACCGCTTCAAGCCACT 409
 Db 339 ACCGCTGCGCGGCTGCGGCTCTGCGGAGAGGAGCGCTTCAACCGCTTCAAGCCACT 398
 QY 410 ATCCGTAAGTCAAGCAAGATGCACTGCGACCCACCATCTGCTGTCAAGCGGAGAG 469
 Db 399 ATCCGTAAGTCAAGCAAGATGCACTGCGACCCACCATCTGCTGTCAAGCGGAGAG 458

QY 470 AGCCCCACCCCTTACAGAGGCGCCCTGACACCCCTCCAGCTTCCGGAACCCCGACAGAGCTGG 529
 Db 459 AGCCCCACCCCTTACAGAGGCGCCCTGACACCCCTCCAGCTTCCGGAACCCCGACAGAGCTGG 518
 QY 530 AACTGAACCGGAGTCCGTGCGGACACCCCAACAGAACATCTTGAACATGACCTGA 589
 Db 519 AACTGAACCGGAGTCCGTGCGGACACCCCAACAGAACATCTTGAACATGACCTGA 578
 QY 590 TGGATAGTGCAGAGCTGGGCGGCGCCCTGACCCCTCCAGCACTTAAGTGGGATCAGGCGCA 649
 Db 579 TGGATAGTGCAGAGCTGGGCGGCGCCCTGACCCCTCCAGCACTTAAGTGGGATCAGGCGCA 638
 QY 650 CGTGCTACGCGACAGCGGCGGCGATGAGAGGCGCGCCCACTTACAGGAGATCATCG 709
 Db 639 CGTGCTACGCGACAGCGGCGGCGATGAGAGGCGCGCCCACTTACAGGAGATCATCG 698
 QY 710 GCCACTACCCGGGTCCTCTTCCAGACACAGACAGATGAGGCGGCTCTTGTCTGG 769
 Db 699 GCCACTACCCGGGTCCTCTTCCAGACACAGACAGATGAGGCGGCTCTTGTCTGG 758
 QY 770 AGGGAGCCCGGCTCCACCAACAACATCGCGCCCTTAGAGAGCGGACCATCTGAGCA 829
 Db 759 AGGGAGCCCGGCTCCACCAACAACATCGCGCCCTTAGAGAGCGGACCATCTGAGCA 818
 QY 830 AAGAGAGATTAACAGAAAGAGACCCCTCTC 861
 Db 819 AAGAGAGATTAACAGAAAGAGACCCCTCTC 850

RESULT 12

US-10-434-479-1
 ; Sequence 1, Application US/10434479
 ; Publication No. US20040092469A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SRIVASTAVA, SHIV
 ; APPLICANT: MOULI, JUDDA W.
 ; APPLICANT: XU, LINDA L.
 ; TITLE OF INVENTION: ANDROGEN-REGULATED PHEPAl GENE AND POLYPEPTIDES
 ; FILE REFERENCE: 04995.0057-02000
 ; CURRENT APPLICATION NUMBER: US/10/434,479
 ; PRIOR FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: 10/390,045
 ; PRIOR FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: 09/769,482
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,772
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,045
 ; PRIOR FILING DATE: 2000-01-31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1140
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (95)..(850)
 ; US-10-434-479-1

Query Match 87.3%; Score 752; DB 17; Length 1140;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 CGGAGCTGAGATTGTTCAATCATCATCTGCTGTGATGATGATGATGATGATG 169
 Db 99 CGGAGCTGAGATTGTTCAATCATCATCTGCTGTGATGATGATGATGATGATG 158
 QY 170 TGATCAAGTGCCTGCTGACGACATCAAGCTGTCTGACGCTCTTATACGCCGACA 229
 Db 159 TGATCAAGTGCCTGCTGACGACATCAAGCTGTCTGACGCTCTTATACGCCGACA 218
 QY 230 GCCAGGGCGGAGAGAGAGATGCTCTGCTCTCAAGAGATGCTGTGCGCTCGAGA 289

Db	219	GCACAGGGGCGGAGAGAGAAAGATGGCTGTCTCTCAAGAGATGGCTGTGGCTTCGAGAGA	278
Qy	290	GCAcAGTGTcAGGcCAAcGGAATccCAAGcCGcCAGGTCTAcGccCGCTTcGgCCcCAcCG	349
Db	279	GCAcAGTGTcAGGcCAAcGGAATccCAAGcCGcCAGGTCTAcGccCGCTTcGgCCcCAcCG	338
Qy	350	ACCGcCTGTGGcCGTGTGGcCGCTTcTGGcCGcCAGcGGAGcGGTCTTcCAcCGCTTcCAAGcCCAcCT	409
Db	339	ACCGcCTGTGGcCGTGTGGcCGCTTcTGGcCGcCAGcGGAGcGGTCTTcCAcCGCTTcCAAGcCCAcCT	398
Qy	410	ATccGTAcCTTcCAcGAcCGAcGATTCGAcCTGTGCcAcCCAcCATcTcGTGTcGAcCGGGAGG	469
Db	399	ATccGTAcCTTcCAcGAcCGAcGATTCGAcCTTcGAcCCAcCATcTcGTGTcGAcCGGGAGG	458
Qy	470	AGcCCcCAcCCCTAcCAcGAGcGGcCGcCTTcGAcCCCTcCAcGCTTcCGGAGcCCcGAGcCAcGAcCTGG	529
Db	459	AGcCCcCAcCCCTAcCAcGAGcGGcCGcCTTcGAcCCCTcCAcGCTTcCGGAGcCCcGAGcCAcGAcCTGG	518
Qy	530	AAcCTGAACcCGGGAGcGTcCGGTGTGGcCGcAcCCcCCAAAcGAAAcCATcTTTcCAcAGTAcCTGA	589
Db	519	AAcCTGAACcCGGGAGcGTcCGGTGTGGcCGcAcCCcCCAAAcGAAAcCATcTTTcCAcAGTAcCTGA	578
Qy	590	TGATATGATGcCAGcGGCTGTGGcCGGcCGcCTcCGcCCcCCcCAGAcGTAAcTTcGGGcCATcCAGcCGcCA	649
Db	579	TGATATGATGcCAGcGGCTGTGGcCGGcCGcCTcCGcCCcCCcCAGAcGTAAcTTcGGGcCATcCAGcCGcCA	638
Qy	650	CGTcCTAcCGcCAGcCGcCGcCGGcCGAcTGAAGGGcCGcCGcCCAcCTAcCAcGAcGAGGTcATcCG	709
Db	639	CGTcCTAcCGcCAGcCGcCGcCGGcCGAcTGAAGGGcCGcCGcCCAcCTAcCAcGAcGAGGTcATcCG	698
Qy	710	GCcAcTAcCCcGGcGGCTcCTTcCTTcTCCAcGAcAcCAGcAGAcGATGTGGcCGcCGCTTcCTTGTcGG	769
Db	699	GCcAcTAcCCcGGcGGCTcCTTcCTTcTCCAcGAcAcCAGcAGAcGATGTGGcCGcCGCTTcCTTGTcGG	758
Qy	770	AGGGAGcCCcGGcCTcCAcCAcCAcCAcATcCGcGGcCGcCTAcGAGcGGcCAGcCAcTTcGAGcCA	829
Db	759	AGGGAGcCCcGGcCTcCAcCAcCAcCAcCAcATcCGcGGcCGcCTAcGAGcGGcCAGcCAcTTcGAGcCA	818
Qy	830	AAAGAAAGATAAcAGAAAGAcCAcCCCTTcC	861
Db	819	AAAGAAAGATAAcAGAAAGAcCAcCCCTTcC	850
RESULT 13			
US-10-205-823-412			
: Sequence 412, Application US/10205823			
: Publication No. US20030108963A1			
GENERAL INFORMATION:			
: APPLICANT: Schlegel, Robert			
: APPLICANT: Monahan, John E.			
: APPLICANT: Endege, Wilson O.			
: APPLICANT: Gannavarapu, Manjula			
: APPLICANT: Gorbacheva, Bella			
: APPLICANT: Hoersch, Sebastian			
: APPLICANT: Kamatekar, Shubhangi			
: APPLICANT: Monsey, Angela M.			
: APPLICANT: Glatt, Karen			
: APPLICANT: Zhao, Xumei			
: APPLICANT: Anderson, Dustin			
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND			
: TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND			
: FILE REFERENCE: MRI-044			
: CURRENT APPLICATION NUMBER: US/10/205, 823			
: CURRENT FILING DATE: 2002-07-25			
: PRIOR APPLICATION NUMBER: 60/307, 982			
: PRIOR FILING DATE: 2001-07-25			
: PRIOR APPLICATION NUMBER: 60/314, 356			
: PRIOR FILING DATE: 2001-08-22			
: PRIOR APPLICATION NUMBER: 60/325, 020			
: PRIOR FILING DATE: 2001-09-25			
: PRIOR APPLICATION NUMBER: 60/341, 746			

```

; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-205-823-412

Query Match      87.3%; Score 752; DB 15; Length 1141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 110 CGAGAGCTGAGATTGTTTCAGATCATCATCATCTGTGTGTGTATGATGATGTGTGTGG 169
DB 100 CGAGAGCTGAGATTGTTTCAGATCATCATCATCTGTGTGTGTATGATGATGTGTGTGG 159
QY 170 TGAATCACTGCTCTGTGTAGCCATCAAGACTGTCTGTGCAACGCTCTTTCATCAAGCCGGGACA 229
DB 160 TGAATCACTGCTCTGTGTAGCCATCAAGACTGTCTGTGCAACGCTCTTTCATCAAGCCGGGACA 219
QY 230 GCCAGGGGCGAGAGAGAGAAATGAGCCCTGTCTCTCAAGAGATGCTGTGGCCCTCGAGAA 289
DB 220 GCCAGGGGCGAGAGAGAGAAATGAGCCCTGTCTCTCAAGAGATGCTGTGGCCCTCGAGAA 279
QY 290 GCACAGTGTCAAGGCACGGAATCCCAAGACCGCAGAGTCTACGCCCCGCTGTGGCCCAACCG 349
DB 280 GCACAGTGTCAAGGCACGGAATCCCAAGACCGCAGAGTCTACGCCCCGCTGTGGCCCAACCG 339
QY 350 ACCGCTGTGGCTGTGCTGCGCTTTCGCGCCCAAGGGGAGAGCTTTCACGCTTTCAGGCCCACT 409
DB 340 ACCGCTGTGGCTGTGCTGCGCTTTCGCGCCCAAGGGGAGAGCTTTCACGCTTTCAGGCCCACT 399
QY 410 ATCGGTACCTGTGACGACGAGATTCGACCTGCGACCCACCAACCATCTGCTGTCAAGCGGGAGAG 469
DB 400 ATCGGTACCTGTGACGAGATTCGACCTGCGACCCACCAACCATCTGCTGTCAAGCGGGAGAG 459
QY 470 AGCCCCCACTTACAGAGGCCCTCTGCAACCTTCAGCTTTCGAGATCCCGAGCAGCAGCTGG 529
DB 460 AGCCCCCACTTACAGAGGCCCTCTGCAACCTTCAGCTTTCGAGATCCCGAGCAGCAGCTGG 519
QY 530 AACTGAACCGGGAGTGGTGTGCGCGCAATCCCAACAGAAACCATCTTTCAGACTGAACCTGA 589
DB 520 AACTGAACCGGGAGTGGTGTGCGCGCAATCCCAACAGAAACCATCTTTCAGACTGAACCTGA 579
QY 590 TGGATTAATGCTCAGAGCTGTGGCGGCGCCCTGCGCCCAAGAGATTAATCGGGGACATCAACGGCA 649
DB 580 TGGATTAATGCTCAGAGCTGTGGCGGCGCCCTGCGCCCAAGAGATTAATCGGGGACATCAACGGCA 639
QY 650 CGTACTACGCGCAGCGCGGCGGCGCATGTGAGGGGCGCGCCCACTCAAGCGAGGATCATCG 709
DB 640 CGTACTACGCGCAGCGCGGCGGCGCATGTGAGGGGCGCGCCCACTCAAGCGAGGATCATCG 699
QY 710 GCCACTACCGCGGGGTCTCTCTTTCAGACACACAGCAGAGGATGGGTCGCTCTTCTGTGG 769
DB 700 GCCACTACCGCGGGGTCTCTCTTTCAGACACACAGCAGAGGATGGGTCGCTCTTCTGTGG 759
QY 770 AGGGGATCCCGGCTTCCACACACACACATCGGGCCCTTGAAGAGCGCAGCATCTGGAGCA 829
DB 760 AGGGGATCCCGGCTTCCACACACACACATCGGGCCCTTGAAGAGCGCAGCATCTGGAGCA 819
QY 830 AAGAGAGGATTAACAGAAAGAGCACCCTTC 861
DB 820 AAGAGAGGATTAACAGAAAGAGCACCCTTC 851

RESULT 14
US-10-301-822-208
; Sequence 208, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:

```


Query Match	87.3%	Score 752	DB 15	Length 1141
Best Local Similarity	100.0%	Pred. NO	0	
Matches 752	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

[illegible]


```
Db      ||||||| 520 AACTGAACCGGAGTCGTCGCGCACCCCAACAGAACCATCTTGACAGTGACCTGA 579
Qy      ||||||| 590 TGGATAGTGCAGGCTGGGCGGCCCCCTGCCCCCAGCAGTAACTCGGCATCAGCGCA 649
Db      ||||||| 580 TGGATAGTGCAGGCTGGGCGGCCCCCTGCCCCCAGCAGTAACTCGGCATCAGCGCA 639
Qy      ||||||| 650 CGTGCTACGCGCAGCGGCGGCGCATGAGAGGCGCGCCCACTACAGCGAGTCAATCG 709
Db      ||||||| 640 CGTGCTACGCGCAGCGGCGGCGCATGAGAGGCGCGCCCACTACAGCGAGTCAATCG 699
Qy      ||||||| 710 GCCACTACCGGCGGCTCTCTTCCAGCACAGCAGAGCATGGGCGGCTCTTGTCTGG 769
Db      ||||||| 700 GCCACTACCGGCGGCTCTCTTCCAGCACAGCAGAGCATGGGCGGCTCTTGTCTGG 759
Qy      ||||||| 770 AGGGGACCGGCTCCACACACACATCGGCGCCCTAGAGAGCGCAGCCATCTGAGCA 829
Db      ||||||| 760 AGGGGACCGGCTCCACACACACATCGGCGCCCTAGAGAGCGCAGCCATCTGAGCA 819
Qy      ||||||| 830 AAGAGAAGATAAACAGAAAGACACCCCTCTC 861
Db      ||||||| 820 AAGAGAAGATAAACAGAAAGACACCCCTCTC 851
```

Search completed: February 20, 2005, 02:39:13
Job time : 485.77 secs

This Page Blank (uspto)

1	693	80.5	901.3	CR612083	full - lens
2	614	71.3	967.5	B0641849	AGENCCOURR
3	566	65.7	1046.5	B0922276	AGENCCOURR
4	558	64.8	609.5	B0635742	AGENCCOURR
5	550	63.9	551.4	BM141979	full
6	536	62.3	605.7	CV028567	full
7	511	59.3	850.5	B0602918	AGENCCOURR
8	499	58.0	916.5	B0954555	AGENCCOURR
9	497	57.7	890.5	B0690750	AGENCCOURR
10	485	56.3	850.1	AL558881	AL558881
11	474	55.1	572.5	BK641317	DXFZP0866
12	470	54.6	729.5	B0575741	UI-H - E21 -
13	449	52.1	945.5	B0539219	AGENCCOURR
14	439	51.0	780.9	AY419334	Homo sapi
15	425	49.4	897.1	AL558882	AL558882
16	424	49.2	1038.1	AL517150	AL517150
17	420	48.8	655.5	B0691705	AGENCCOURR
18	420	48.4	1280.5	B0691500	AGENCCOURT
19	417	48.4	782.5	B0015170	UI-H - ED1 -
20	402	46.7	964.5	B0859860	AGENCCOURR
21	394	45.8	602.6	CA431191	UI-H - FG1 -
22	393	45.6	461.4	BM712680	UI-E - BJO -
23	390	45.3	973.5	BM165156	AGENCCOURR
24	389	45.2	633.4	BM714472	UI-E - BJO -

C	25	380	44.1	588	5	B0624784	UI-H-FGI-
C	26	374	43.4	549	5	B0686793	B0686793 AGENCOURT
C	27	374	43.4	938	5	BUI57842	BUI57842 AGENCOURT
C	28	374	41.4	952	5	BUI57859	BUI57859 AGENCOURT
C	29	369	42.9	559	2	BE855409	BE855409 7g13f05. x
C	30	369	41.9	629	5	BUI730650	BUI730650 UI-E-CIT-
C	31	358	41.6	1127	5	BUI74654	BUI74654 AGENCOURT
C	32	353	41.0	730	4	BM677662	BM677662 UI-E-EOL-
C	33	351	40.8	626	5	BM974436	BM974436 UI-CF-EC1
C	34	347	40.3	528	7	CN296134	CN296134 170006001
C	35	345	40.1	744	5	B0683523	B0683523 UI-CF-EC1
C	36	335	38.9	570	5	B057582	B057582 UI-H-EZ1-
C	37	331	38.4	899	5	BUI96812	BUI96812 AGENCOURT
C	38	330	38.3	552	4	BM113500	BM113500 UI-E-EJO-
C	39	329	38.2	563	6	CB049800	CB049800 NISC_gj13
C	40	302	35.1	651	6	CB554226	CB554226 MBSP0052-
C	41	302	35.1	693	1	A1761441	A1761441 wgsfE07. x
C	42	300	34.8	646	5	B0659841	B0659841 AGENCOURT
C	44	290	33.7	867	5	BX362396	BX362396 BX362396
C	44	279	33.4	547	4	BM676516	BM676516 UI-E-EJO-
C	45	277	32.2	277	6	CB108549	CB108549 K-ESP0148

ALIGNMENTS

RESULT 1

CR612083
LOCHE

DEFINITION

ACCESSION
NUMBER

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

JOURNAL
DEMARBY

2

REFERENCE

TITLE
FORMAT

COMMENT

FRAMPTON

Source

ORIGIN

Query Ma
Post-100

Matches

QY

169 GTGATCAGTGCCTGCTGAGCCACTACAAGCTGTCTGCACGGTCTTCATCAGCCGGCAC 228


```

Db      1 GTGATCACTGCTCTGAGCCATCAAGTGTCTGACGAGCTCTTCATCAGCCGCGAC 60
Qy      229 AGCCAGGGGCGGAGGAGGAGGAGATGCGCTGTCTCTAGAGAGATGCTGTGGCCCTCGAG 288
Db      61 AGCCAGGGGCGGAGGAGGAGGAGATGCGCTGTCTCTAGAGAGATGCTGTGGCCCTCGAG 120
Qy      289 AGCAGAGTGTCAAGGAGGAGGAGATGCGAGAGCCGAGGCTTCAAGCCGCTCGAGCCAGC 348
Db      121 AGCAGAGTGTCAAGGAGGAGGAGATGCGAGAGCCGAGGCTTCAAGCCGCTCGAGCCAGC 180
Qy      349 GAGCCGCTGCGGCTGCGGCTCTTCTGCGGAGGAGGAGGCTTCAAGCCGCTCGAGCCAGC 408
Db      181 GAGCCGCTGCGGCTGCGGCTCTTCTGCGGAGGAGGAGGCTTCAAGCCGCTCGAGCCAGC 240
Qy      409 TATCCGTACTGAGCAGAGAGATGCACTTGCACCAACATCTGCTGTGAGAGGGAG 468
Db      241 TATCCGTACTGAGCAGAGATGCACTTGCACCAACATCTGCTGTGAGAGGGAG 300
Qy      469 GAGCCGCTGAGCAGGAGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 528
Db      301 GAGCCGCTGAGCAGGAGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 360
Qy      529 GAATCTGAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db      361 GAATCTGAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy      589 ATGATAGTGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 648
Db      421 ATGATAGTGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy      649 AGTGTCTACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 708
Db      481 AGTGTCTACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Qy      709 GGGCACTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 768
Db      541 GGGCACTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Qy      769 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 828
Db      601 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy      829 AAAGAGAGGATTAACAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 861
Db      661 AAAGAGAGGATTAACAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 693

```

RESULT 2
BO641849 967 bp mRNA linear EST 15-JUN-2002
LOCUS AGENCOURT 8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
DEFINITION 5', mRNA sequence.
ACCESSION BO641849
VERSION BO641849.1 GI:21766021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 967)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: sgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Robin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LINCW493 row: 9 column: 18

High quality sequence stop: 571.
Location/Qualifiers
1. 967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6292265"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_43"
/note="Organ: eye; Vector: pOT7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 71.3%; Score 614; DB 5; Length 967;
Best Local Similarity 99.7%; Pred. No. 6.5e-298;
Matches 714; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      112 GAGCTGAGTTTGTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 171
Db      1 GAGCTGAGTTTGTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 60
Qy      172 ATGACGTGCTGCTGAGCCATCAAAAGTGTGTGACGCTCTTCAATCAAGCCGAGCAGC 231
Db      61 ATGACGTGCTGCTGAGCCATCAAAAGTGTGTGACGCTCTTCAATCAAGCCGAGCAGC 120
Qy      232 CAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 291
Db      121 CAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy      292 ACAGTGTCAAGCAAGGAAATCCAGAGCCGAGGTCTAGCCGCTCGGCTCGGCAACGAG 351
Db      181 ACAGTGTCAAGCAAGGAAATCCAGAGCCGAGGTCTAGCCGCTCGGCTCGGCAACGAG 240
Qy      352 CGCTTGGCGGTGCGGCTCTTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 411
Db      241 CGCTTGGCGGTGCGGCTCTTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy      412 CCGTACCTGAGCAGAGATGCACTGACCTGCCACCAACATCTGCTGTGAGAGGAGGAGGAG 471
Db      301 CCGTACCTGAGCAGAGATGCACTGACCTGCCACCAACATCTGCTGTGAGAGGAGGAGGAG 360
Qy      472 CCCCACCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 531
Db      361 CCCCACCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy      532 CTGAAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
Db      421 CTGAAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy      592 GATATGTGCAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 651
Db      481 GATATGTGCAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Qy      652 TGTCTAGGAGCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 711
Db      541 TGTCTAGGAGCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Qy      712 CACTTACCGGAGTGTCTTCTTCAAGCAGCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 771
Db      601 CACTTACCGGAGTGTCTTCTTCAAGCAGCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Qy      772 GGGAGCCGAGCTCAACACACACACATCGGCGCCCTTGAAGAGGAGGAGGAGGAGGAGGAGGAG 827
Db      661 GGGAGCCGAGCTCAACACACACACATCGGCGCCCTTGAAGAGGAGGAGGAGGAGGAGGAGGAG 716

```


Df		367	GGCAAGGAAATCCAGAGCGCAGAGTCTACGCCGCCCTCGGCACCACGACCGCCTG3CC	426
OY		361	GTEGCCGCCCTTGCGCCACAGCGGAGCGCTTCACACGGCTTCAGGCCCACTTATCGGTACTG	420
Df		427	GTGCGCGCCCTTGCGCCACAGCGGAGCGCTTCACACGGCTTCAGGCCCACTTATCGGTACTG	486
OY		421	CAGACAGAGATTCAGCTGCGCACCCACCATCTCGCTGTGCAGCGGGGAGGAGCCCCAACCC	480
Df		487	CAGACAGAGATTCAGCTGCGCACCCACCATCTCGCTGTGCAGCGGGGAGGAGCCCCAACCC	546
OY		481	TACCAAGGCGCCCTTCACACCTTCAGCTTCGGAACCCGAGCAGCAGTGGAACTGAACCGG	540
Df		547	TACCAAGGCGCCCTTCACACCTTCAGCTTCGGAACCCGAGCAGCAGTGGAACTGAACCGG	606
OY		541	GAGTCGTGCGCGCAGCACCCCAAACAACCATCTTTGACAGTGCATTGATGATGTCGCC	600
Df		607	GAGTCGTGCGCGCAGCACCCCAAACAACCATCTTTGACAGTGCATTGATGATGTCGCC	666
OY		601	AGGCTGGGCGCGCCCTCTGCCGCCCGACGATTAATCTCGGSCAATCAGCGCAGCTGTACGCG	660
Df		667	AGGCTGGGCGCGCCCTCTGCCGCCCGACGATTAATCTCGGSCAATCAGCGCAGCTGTACGCG	726
OY		661	AGCGGCGG 668	
Df		727	AGCGGCGG 734	
RESULT 4				
B0636742				
LOCUS				
DEFINITION		609 bp mRNA linear EST 15-JUN-2002		
DESCRIPTION		hd13h06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he		
ACCESSION		B0636742		
VERSION		B0636742.1 GI:21761201		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 609)		
REFERENCE		Mistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.A., Expressed sequence tag analysis of human retina for the NEIBank Project: Rebinding, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts Mol. Vis. 8 (4), 196-204 (2002)		
JOURNAL		22103461		
MEDLINE		12107411		
PUBMED		Contact: Mistow G		
COMMENT		Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 13 row: h column: 06 Seq primer: M13RPI reverse primer (ABI).		
FEATURES		Location/Qualifiers		
SOURCE		1..609		
		/organism="Homo sapiens"		
		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/clone="hd13h06"		
		/tissue_type="Retina"		
		/dev_stage="Adult"		
		/lab_host="EMDHI0B"		
		/clone_id="Human Retina cDNA (Un-normalized, unamplified)": hd/he"		
		/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directional cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at		

Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTAGTCTAGATTCGGACGGCCGCC(T)15-3'). EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 64.8%; Score 558; DB 5; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.1e-269;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

219 CAGCCGCGACAGCCGCGGCGGAGAGAGATGCCCTGTCAGAGAGATGCTGTG 278
1 CAGCCGCGACAGCCGCGGCGGAGAGAGATGCCCTGTCAGAGAGATGCTGTG 60
279 GCCCTCGAGAGACAGTGTCTAGGCAACGGAATCCAGAGCCGCAAGTCTAAGCCCGCC 338
61 GCCCTCGAGAGACAGTGTCTAGGCAACGGAATCCAGAGCCGCAAGTCTAAGCCCGCC 120
339 TCGCCCAACGAGCCGCTGCGCGCTGCGCCCTTCCAGAGGCGGAGCGCTTCAACCGCTT 398
121 TCGCCCAACGAGCCGCTGCGCGCTGCGCCCTTCCAGAGGCGGAGCGCTTCAACCGCTT 180
399 CCAGCCCACTATCCGTAACCTGACAGAGATGCACTGCGACCAACATCTGCTGTC 458
181 CCAGCCCACTATCCGTAACCTGACAGAGATGCACTGCGACCAACATCTGCTGTC 240
459 AGACGGGGAGAGAGCCCGCACTTACAGAGGCGCTTCAACCTTCCAGCTTGGAGACCCGA 518
241 AGACGGGGAGAGAGCCCGCACTTACAGAGGCGCTTCAACCTTCCAGCTTGGAGACCCGA 300
519 GCAGAGCTGGAAGTGAACGCGGAGTGGTGGGAGACCCCAAGAGAGATCTTGA 578
301 GCAGAGCTGGAAGTGAACGCGGAGTGGTGGGAGACCCCAAGAGAGATCTTGA 360
579 CAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 638
361 CAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
639 CATAGAGGCGCACTGTAACGCGGAGTGGTGGGAGACCCCAAGAGAGATCTTGA 698
421 CATAGAGGCGCACTGTAACGCGGAGTGGTGGGAGACCCCAAGAGAGATCTTGA 480
699 CGAGGTATCGGCGCACTGTAACGCGGAGTGGTGGGAGACCCCAAGAGAGATCTTGA 758
481 CGAGGTATCGGCGCACTGTAACGCGGAGTGGTGGGAGACCCCAAGAGAGATCTTGA 540
759 CTCTTGTGAGAGGAGACCCGCTTCAACAGACATGCGCGCTTGAAGAGCGGAGC 818
541 CTCTTGTGAGAGGAGACCCGCTTCAACAGACATGCGCGCTTGAAGAGCGGAGC 600
819 CATCTGAG 827
601 CATCTGAG 609

RESULT 5
BM141979
LOCUS
DEFINITION
BM141979 551 bp mRNA linear EST 12-MAR-2002
1:525a11.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5677341 5' similar to TR:Q9UUD3 Q9UUD3 D71877.1
/, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 551)
Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, D., Marra, M., Pape, D., Wylie, T., Martin, J., Birstein, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvill, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)

JOURNAL

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu

COMMENT

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 429.
Location/Qualifiers
1. .551
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5677341"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
Superscript library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

FEATURES

source

ORIGIN

Query Match 63.9%; Score 550; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 1.2e-265;
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

302 GCAACGGAATCCAGAGCGGAGTCTACGCCCGCTGCGCCACGACGCGCTGCGCG 361
1 GCAACGGAATCCAGAGCGGAGTCTACGCCCGCTGCGCCACGACGCGCTGCGCG 60
362 TGGCGCCCTTGGCGGAGGAGGCGCTTCCACCGCTTCCAGCCCACTATCCGTAACCTGC 421
61 TGGCGCCCTTGGCGGAGGAGGCGCTTCCACCGCTTCCAGCCCACTATCCGTAACCTGC 120
422 AGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 481
121 AGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 180
482 ACCAGGCGCCCTGCAACCTTCCAGCTTGGAGACCCCGAGCAGCTGGAATGAACCGGG 541
181 ACCAGGCGCCCTGCAACCTTCCAGCTTGGAGACCCCGAGCAGCTGGAATGAACCGGG 240
542 AGTGGTGGCGGACCCCAAGAGAGATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 601

ORIGIN	Query Match	62.3%; Score 536; DB 7; Length 605;
	Best Local Similarity 99.8%; Pred. No. 1,4e-258;	
	Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	165 GGTGGTATCATCGTGCCTGCTGAGCCCACTACAGCTGTCTGCAAGGCTCTTCATCAGCCG 224	
DB	15 GGTGTGATCATCGTGCCTGCTGAGCCCACTACAGCTGTCTGCAAGGCTCTTCATCAGCCG 74	
QY	225 GCACAGCCAGGGGCGAGAGAGAAAGTATGCCCTGTCTCTCAGAGAGATGCTGTGCGCCCTC 284	
DB	75 GCACAGCCAGGGGCGAGAGAGAAAGTATGCCCTGTCTCTCAGAGAGATGCTGTGCGCCCTC 134	
QY	285 GGAGAGACAGTGTCAAGGCAACCGGAATCCCAAGACCGCAAGGCTCAAGCGCCCGCTCGGCC 344	
DB	135 GGAGAGACAGTGTCAAGGCAACCGGAATCCCAAGACCGCAAGGCTCAAGCGCCCGCTCGGCC 194	
QY	345 CACCGACCGGCTGGCGCGTGCAGCCCTTCGCGCCAGCGGAGAGGCTTCACAGCTTCCAGCC 404	
DB	195 CACCGACCGGCTGGCGCGTGCAGCCCTTCGCGCGGAGAGGCTTCCACAGCTTCCAGCC 254	
QY	405 CACCTATCCGTAAGCTGAGACAGAGATGACCTTGCCACCCACATCTTGCTGTGACAGCG 464	
DB	255 CACCTATCCGTAAGCTGAGACAGAGATGACCTTGCCACCCACATCTTGCTGTGACAGCG 314	
QY	465 GGAAGAGCCCCCAACCTTACAGAGGCCCCCTGCAACCTTCAAGTTGGGAGCCCGAGCAGCA 524	
DB	315 GGAAGAGCCCCCAACCTTACAGAGGCCCCCTGCAACCTTCAAGTTGGGAGCCCGAGCAGCA 374	
QY	525 GCTGGAACCTGAAACCGGAGTGCAGTGCAGCGACCCCAACAGAACCATCTTCCAGAGTGA 584	
DB	375 GCTGGAACCTGAAACCGGAGTGCAGTGCAGCGACCCCAACAGAACCATCTTCCAGAGTGA 434	
QY	585 CTTGATGATATAGTGCAGGCTGGGCGGCCCTTCGCGCCCAAGAGTAACTTGCGGCATCAG 644	
DB	435 CTTGATGATATAGTGCAGGCTGGGCGGCCCTTCGCGCCCAAGAGTAACTTGCGGCATCAG 494	
QY	645 CGCCACGTGCTACGCGCAGCGCGCGGCGCATGAGAGGGGCGCGCGCCACCTTACAGAGT 704	
DB	495 CGCCACGTGCTACGCGCAGCGCGCGGCGCATGAGAGGGGCGCGCGCCACCTTACAGAGT 554	
QY	705 CATCGGCGACATACCGGGGATCTCTCTTCAGAGCAGCAGAGCAGTG 751	
DB	555 CATCGGCGACATACCGGGGATCTCTCTTCAGAGCAGCAGAGCAGTG 601	
RESULT 7		
BU602918	850 bp	mRNA
LOCUS	AGENCOURT_10016502 NIH_MGC_142 Homo sapiens	linear
DEFINITION	IMAGE:6497853 5', mRNA sequence.	EST 20-SEP-2002
ACCESSION	BU602918	
VERSION	BU602918.1	
KEYWORDS	GI:23254677	
SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Homo sapiens	
AUTHORS	Emkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
JOURNAL	1 (bases 1 to 850)	
COMMENT	NIH-MGC http://mgs.nci.nih.gov/	
	National Institutes of Health, Mammalian Gene Collection (MGC)	
	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgabs-remail.nih.gov	
	Tissue Procurement: NCI	
	CDNA Library Preparation: Michael Brownstein Laboratory	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIMU)	
	DNA Sequencing by: Agencourt Bioscience Corporation	


```

17:organism="Homo sapiens"
18:mol_type="RNA"
19/db_xref="taxon:9606"
20:clone_image=6209341"
21:tissue_image="ductal carcinoma, cell line"
22/lab_host="DH10B (phage-resistant)"
23:/clone.lib="NH_MGC_110"
24:note="Organ: pancreas; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the
```

Matches	547:	Conservative	0:	Mismatches	1:	Indels	0:	Gaps	0:
QY	110	CGAGCTGGAATTGTTCAATCATCATCATCTGCTGCTGATGATGATGATGATGCTG	169						
Db	128	CGAGCTGGAATTGTTCAATCATCATCATCTGCTGCTGATGATGATGATGATGCTG	187						
QY	170	TGATCAGTGGCTCTGCTGACCACTAACAGCTGTCTGACCGTCTTTCATCAGCCGGACA	229						
Db	188	TGATCAGTGGCTCTGCTGACCACTAACAGCTGTCTGACCGTCTTTCATCAGCCGGACA	247						
QY	230	GCACGGGGCGGAGAGAGATGCGCTGCTCAGAAAGATGCTGCGCCCTCGAGAGA	289						
Db	248	GCACGGGGCGGAGAGAGATGCGCTGCTCAGAAAGATGCTGCGCCCTCGAGAGA	307						
QY	290	GCACAGTGTCAAGGCAACGGAATCCACAGCGCGAGTCTACGCCCGCTCGGCCACCG	349						
Db	308	GCACAGTGTCAAGGCAACGGAATCCACAGCGCGAGTCTACGCCCGCTCGGCCACCG	367						
QY	350	ACCGCTTGCGCGCTGCGCCCTTTCGCGGAGCGGAGCGCTTTCACCGCTTTCAGCTCACT	409						
Db	368	ACCGCTTGCGCGCTGCGCCCTTTCGCGGAGCGGAGCGCTTTCACCGCTTTCAGCTCACT	427						
QY	410	ATCCGTACCTGACACAGATTCGACCTTGCACCCACATTCGCTGTCAGACGGGGAGG	469						
Db	428	ATCCGTACCTGACACAGATTCGACCTTGCACCCACATTCGCTGTCAGACGGGGAGG	487						
QY	470	AGCCCCACCTTACAGAGGCCCTTGCACACCTTCAGCTTTCGGGACCCGAGAGAGAGCTGG	529						
Db	488	AGCCCCACCTTACAGAGGCCCTTGCACACCTTCAGCTTTCGGGACCCGAGAGAGAGCTGG	547						
QY	530	AACCTGAACCGGAGAGTGGGTGGCGCACCCCCCAACAGAACCATCTTTCAGACGTGACCTGA	589						
Db	548	AACCTGAACCGGAGAGTGGGTGGCGCACCCCCCAACAGAACCATCTTTCAGACGTGACCTGA	607						
QY	590	TGATAGTGGCAGGCTGGGGCGGCGCCCTTTCGCCCCCAGACGTAATCTCGGGCATCAGCGCCA	649						
Db	608	TGATAGTGGCAGGCTGGGGCGGCGCCCTTTCGCCCCCAGACGTAATCTCGGGCATCAGCGCCA	667						
QY	650	CGTGTCTAC 657							
Db	668	CGTGTCTAC 675							
RESULT 10									
AL558881/c									
LOCUS									
DEFINITION									
AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED									
ACCESSION									
AL558881 Homo sapiens cDNA clone CS00D015F12 3-PRIME, mRNA sequence.									
VERSION									
AL558881.3 GI:46184268									
KEYWORDS									
EST.									
SOURCE									
ORGANISM									
Homo sapiens (human)									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
REFERENCE									
AUTHORS									
L4,W.B., Gruber,C., Jeasee,J. and Polayes,D.									
TITLE									
Full-length cDNA libraries and normalization									
JOURNAL									
Unpublished (2001)									

1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdnas/CS0D015D06NP1&c=9945.r>.

FEATURES

source

```
1. 850
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D015D06NP1"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

Query Match 56.3%; Score 485; DB 1; Length 850;

Best Local Similarity 99.4%; Pred. No. 6.9e-233; Matches 685; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 173 TCACGTGCTGCTGAGCCATCAAGCTGTGACGGCTCTTATACAGCCGACAGCC 232
DB 173 TCACGTGCTGCTGAGCCATCAAGCTGTGACGGCTCTTATACAGCCGACAGCC 232
QY 846 TCAGTGTCTCTGAGCCATCAAGCTGTGACGGCTCTTATACAGCCGACAGCC 787
DB 846 TCAGTGTCTCTGAGCCATCAAGCTGTGACGGCTCTTATACAGCCGACAGCC 787
QY 233 AGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 292
DB 233 AGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 292
QY 786 AGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
DB 786 AGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
QY 293 CAGTGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 352
DB 293 CAGTGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 352
QY 726 CAGTGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
DB 726 CAGTGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
QY 353 GCCTGCGCGTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
DB 353 GCCTGCGCGTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 666 GCCTGCGCGTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
DB 666 GCCTGCGCGTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
QY 413 CGTACTGACAGCAGAGATGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
DB 413 CGTACTGACAGCAGAGATGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
QY 606 CGTACTGACAGCAGAGATGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
DB 606 CGTACTGACAGCAGAGATGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
QY 473 CCCCACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
DB 473 CCCCACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
QY 546 CCCCACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
DB 546 CCCCACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
QY 533 TGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 592
DB 533 TGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 592
QY 486 TGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB 486 TGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
QY 593 ATAGTGCAGAGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
DB 593 ATAGTGCAGAGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
QY 426 ATAGTGCAGAGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
DB 426 ATAGTGCAGAGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
QY 653 GCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 712
DB 653 GCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 712
QY 366 GCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
DB 366 GCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
QY 713 ACTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772
DB 713 ACTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772
QY 306 ACTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247
DB 306 ACTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247
QY 773 GGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
DB 773 GGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
QY 246 GGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187
DB 246 GGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187
QY 833 AGAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
DB 833 AGAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
```

Db 186 AGAAGATTAAG 158

RESULT 11

EX641317

LOCUS

DEFINITION DXFZp686K23134 r1 686 (synonym: hlc03) Homo sapiens CDNA clone

ACCESSION

EX641317

VERSION

EX641317.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

MIPS

INGOLSTADTER Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;

Heidelberg/Germany) within the CDNA sequencing consortium of the

German Genome Project.

No s1 sequence available.

This clone (DXFZp686K23134) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

Location/Qualifiers

1. 572

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DXFZp686K23134"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: hlc03)"

/note="Vector: pTriplEx2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

ORIGIN

Query Match 55.1%; Score 474; DB 5; Length 572;

Best Local Similarity 99.8%; Pred. No. 2.4e-227;

Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 258 GTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 317
DB 258 GTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 317
QY 1 GTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 1 GTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 318 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 377
DB 318 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 377
QY 61 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 378 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 437
DB 378 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 437
QY 121 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 438 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 497
DB 438 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 497
QY 181 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GCGGAGAGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 498 CCTTCAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
DB 498 CCTTCAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
QY 241 CCTTCAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 CCTTCAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
```


This Page Blank (uspto)